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OM protein - protein search, using sw model

Run on: April 22, 2003, 17:11:26 ; Search time 36 Seconds

(without alignments)
932.754 Million cell updates/sec

Title: US-09-910-033a-2

Perfect score: 1290

Sequence: 1 MSNRLDGKVAITGTGTLGIG.....NESKATGSEFVVDGVTAA 252

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq-101002:*

1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
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22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1290	100.0	252	23	AAO16940
2	1277	99.0	252	18	AAW23407
3	1019	79.0	251	18	AAW23409
4	456	35.3	254	22	AAW49773
5	450	34.9	254	22	AAW47522
6	400	31.0	258	21	AAW56815
7	376	29.1	257	23	ABP38717
8	369	28.6	272	22	AAU37095
9	368	28.5	253	23	ABW54214
10	367.5	28.5	261	13	AAW27757

11	366.5	28.4	261	23	AAE20115	Lactobacillus rham
12	364.5	28.3	261	11	AAW04044	Glucose dehydrogen
13	364.5	28.3	261	13	AAW24018	Thermostable gluc
14	364	28.2	251	22	AAU34193	Staphylococcus aur
15	363.5	28.2	272	21	AAW10740	B. megaterium gluc
16	363.5	28.2	340	21	AAW10741	H. ghiliana11/B. me
17	360.5	27.9	261	11	AAW03846	Modified glucose d
18	359.5	27.9	261	13	AAW27756	NAD affinity glucos
19	358.5	27.8	261	9	AAW05090	Sequence of glucos
20	358.5	27.8	261	21	AAW96271	B. subtilis glucos
21	358.5	27.8	261	21	AAW54424	Amino acid sequenc
22	356.5	27.6	261	9	AAW80063	Glucose dehydrogen
23	352.5	27.3	262	22	AAW83032	S. epidermidis ope
24	351	27.2	286	22	AAU36287	Pseudomonas aerugi
25	348.5	26.7	263	23	ABP39667	Staphylococcus epi
26	345	26.7	306	22	AAW81644	S. epidermidis ope
27	344	26.7	270	21	AAW42558	Human ORFX ORF2322
28	344	26.7	303	23	ABW92624	Herbicideally activ
29	341	26.4	274	23	ABP39586	Staphylococcus epi
30	340	26.4	270	20	AAW41761	Human PRO474 prote
31	340	26.4	270	21	AAW44317	Human PRO474 (UNO5
32	340	26.4	270	21	AAW24056	Human PRO474 prote
33	340	26.4	270	22	AAU28108	Novel human secret
34	340	26.4	279	22	AAU18286	Human endocrine po
35	336.5	26.1	271	22	AAU37794	Streptococcus pneu
36	336.5	26.1	272	22	AAU38086	Streptococcus pneu
37	334.5	25.9	288	22	AAU28296	Novel human secret
38	333.5	25.9	280	23	ABW92449	Herbicideally activ
39	330.5	25.6	254	23	ABW30228	Streptococcus poly
40	330.5	25.6	263	23	ABW28167	Streptococcus poly
41	330.5	25.6	270	23	ABW26580	Streptococcus poly
42	330.5	25.6	277	21	AAW54415	Secoisolaricresin
43	324	25.1	253	23	ABW50010	Listeria monocytog
44	324	25.1	274	23	AAW22161	Ramoplanin biosync
45	324	25.1	336	16	AAW06488	Maize 152 sequence

ALIGNMENTS

RESULT 1
AAO16940
AAO16940 standard; Protein: 252 AA.

AAO16940:
16-MAR-2002 (first entry)

Recombinant enzyme with increased NAD(H) acceptance.

NAD(H) acceptance enzyme; reduced nicotinamide-adenine dinucleotide;

ketone; alchoho; enantiomerically enriched.

Unidentified.

Synthetic.

Key Location/Qualifiers

Misc-difference 38 /note- "wild-type Gly substituted by Asp."

EP1176203-A1.
30-JAN-2002.
20-JUN-2001: 2001EP-0114953.
27-JUL-2000: 2000DE-1037101.
(DEGS) DECUSSA AG.
Riebel B, Hummel W, Bommarilus A;
WPI: 2002-173122/23.

DR N-PSDB: AAL45006.

XX New recombinant enzyme, useful for enantioselective synthesis of e.g.
PT alcohols, has increased nicotinamide-adenine dinucleotide acceptance as
PT result of specific mutation

XX Disclosure: Page 7-8; 23pp; German.

CC The present invention relates to a recombinant enzyme with higher NAD(H)
CC (reduced) nicotinamide-adenine dinucleotide) acceptance than the wild
CC type, and which has at least one neutral amino acid exchanged for an
CC acidic amino acid, while retaining the basic amino acid in the co-enzyme
CC binding site. The enzyme can be used to prepare enantioselectively enriched
CC organic compounds, especially enantioselective reduction of ketones or
CC oxidation of alcohols. The present sequence is the enzyme of the
CC invention.

XX Sequence 252 AA:

Query Match 100.0%; Score 1290; DB 23; Length 252;
Best Local Similarity 100.0%; Pred. No. 4,3e-117;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSNRLDGVKVAITITGCTGIGLAIAATKFEVGGAKVMTDRHSDVGEKAAKSVGTPOIOFF 60
DB 1 MSNRLDGVKVAITITGCTGIGLAIAATKFEVGGAKVMTDRHSDVGEKAAKSVGTPOIOFF 60
QY 61 QHDSDEDEGWTKLFDATKAGPSTLVNNGIAVNSVEETTAEMRKLAVNLDGVFF 120
DB 61 QHDSDEDEGWTKLFDATKAGPSTLVNNGIAVNSVEETTAEMRKLAVNLDGVFF 120
QY 121 GTRIGIORMKNKKGASIIINNSIEGFVGPDLGAYNASKAVRIMSKAALDCAKDXYD 180
DB 121 GTRIGIORMKNKKGASIIINNSIEGFVGPDLGAYNASKAVRIMSKAALDCAKDXYD 180
QY 181 VRVNTVHPGYIKTPLVVDLPGAEAMSORRTKTPMGHIGEPNDIAYICVYLANSKSRATG 240
DB 181 VRVNTVHPGYIKTPLVVDLPGAEAMSORRTKTPMGHIGEPNDIAYICVYLANSKSRATG 240
QY 241 SEFVVDGTYTAQ 252
DB 241 SEFVVDGTYTAQ 252

RESULT 2

AAM23407

ID AAM23407 standard; Protein; 252 AA.

XX AAM23407;

DT 27-MAR-1998 (first entry)

XX Lactobacillus brevis alcohol dehydrogenase.

KW Alcohol dehydrogenase; production; (R)-alcohol; (S)-alcohol.

OS Lactobacillus brevis.

PN EP796914-A2.

PD 24-SEP-1997.

PF 20-MAR-1997; 97EP-0104814.

PR 21-MAR-1996; 96DE-4010984.

PA (BOEF) BOEHRINGER MANNHEIM GMBH.

PI Hummel W, Riebel B;

XX WPI; 1997-459831/43.

DR N-PSDB: AAT73132.

XX

PT Lactobacillus brevis alcohol dehydrogenase - useful for production
PT of optically active alcohol(s)

XX Claim 8; Pages 24-26; 34pp; German.

CC The present sequence is a lactobacillus brevis alcohol
CC dehydrogenase, which retains at least 95% of its activity after 30
CC minutes at 20-60 degrees C and can be purified to a specific
CC activity of at least 400 U/mg. The enzyme can be used to produce
CC (R)-alcohols by enantioselective reduction of ketones of formula
CC R1-CO-R2, where R1 and R2 = hydrogen (sic) or 1-20C alkyl, alkenyl,
CC aryl or arylethyl (sic) optionally substituted by halogen, NO2, OH
CC or 1-20C alkoxy, "an optionally substituted 1-10C alkylene group,
CC which is substituted by saturated, unsaturated or aromatic
CC nitrogen, oxygen or sulphur heterocycles, or may be an optionally
CC substituted polycondensed saturated and/or aromatic group" (sic) in
CC the presence of the enzyme or cells containing it at 20-60 degrees
CC C for 0.25-3 hours, or (S)-alcohols by incubating a racemic alcohol
CC of formula R1-CHOH-R2 in the presence of the enzyme or cells
CC containing it at 20-60 degrees C for 0.25-3 hours.

XX Sequence 252 AA:

Query Match 99.0%; Score 1277; DB 18; Length 252;
Best Local Similarity 99.2%; Pred. No. 7,9e-116;
Matches 250; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSNRLDGVKVAITITGCTGIGLAIAATKFEVGGAKVMTDRHSDVGEKAAKSVGTPOIOFF 60
DB 1 MSNRLDGVKVAITITGCTGIGLAIAATKFEVGGAKVMTDRHSDVGEKAAKSVGTPOIOFF 60
QY 61 QHDSDEDEGWTKLFDATKAGPSTLVNNGIAVNSVEETTAEMRKLAVNLDGVFF 120
DB 61 QHDSDEDEGWTKLFDATKAGPSTLVNNGIAVNSVEETTAEMRKLAVNLDGVFF 120
QY 121 GTRIGIORMKNKKGASIIINNSIEGFVGPDLGAYNASKAVRIMSKAALDCAKDXYD 180
DB 121 GTRIGIORMKNKKGASIIINNSIEGFVGPDLGAYNASKAVRIMSKAALDCAKDXYD 180
QY 181 VRVNTVHPGYIKTPLVVDLPGAEAMSORRTKTPMGHIGEPNDIAYICVYLANSKSRATG 240
DB 181 VRVNTVHPGYIKTPLVVDLPGAEAMSORRTKTPMGHIGEPNDIAYICVYLANSKSRATG 240
QY 241 SEFVVDGTYTAQ 252
DB 241 SEFVVDGTYTAQ 252

RESULT 3

AAM23409

ID AAM23409 standard; Protein; 251 AA.

XX AAM23409;

DT 27-MAR-1998 (first entry)

XX Lactobacillus kefir alcohol dehydrogenase.

KW Alcohol dehydrogenase; production; (R)-alcohol; (S)-alcohol.

OS Lactobacillus kefir.

PN Key Location/Qualifiers

FT Misc-difference 46 /note= "not defined in specification"

FT Misc-difference 47 /note= "not defined in specification"

FT Misc-difference 48 /note= "not defined in specification"

FT Misc-difference 49 /note= "not defined in specification"

FT Misc-difference 50 /note= "not defined in specification"

FT Misc-difference 51 /note- "not defined in specification"
 FT Misc-difference 52 /note- "not defined in specification"
 FT Misc-difference 53 /note- "not defined in specification"
 FT Misc-difference 54 /note- "not defined in specification"
 FT Misc-difference 55 /note- "not defined in specification"
 FT Misc-difference 56 /note- "not defined in specification"
 FT Misc-difference 57 /note- "not defined in specification"
 FT Misc-difference 58 /note- "not defined in specification"
 FT Misc-difference 59 /note- "not defined in specification"
 FT Misc-difference 60 /note- "not defined in specification"
 FT Misc-difference 61 /note- "not defined in specification"
 FT Misc-difference 62 /note- "not defined in specification"
 FT Misc-difference 63 /note- "not defined in specification"
 FT Misc-difference 64 /note- "not defined in specification"
 FT Misc-difference 65 /note- "not defined in specification"
 FT Misc-difference 66 /note- "not defined in specification"
 FT Misc-difference 67 /note- "not defined in specification"
 FT Misc-difference 68 /note- "not defined in specification"
 FT Misc-difference 69 /note- "not defined in specification"
 FT Misc-difference 70 /note- "not defined in specification"
 FT Misc-difference 71 /note- "not defined in specification"
 FT Misc-difference 130 /note- "not defined in specification"
 FT Misc-difference 131 /note- "not defined in specification"
 FT Misc-difference 132 /note- "not defined in specification"
 EP796914-A2.
 XX
 PD 24-SEP-1997.
 XX
 PF 20-MAR-1997; 97EP-0104814.
 XX
 PR 21-MAR-1996; 96DE-4010984.
 XX
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 XX
 PI Hummel W, Riebel B;
 XX
 DR WPI; 1997-459831/43.
 XX
 PT Lactobacillus brevis alcohol dehydrogenase - useful for production
 of optically active alcohol(s)
 XX
 PS Example 8; Pages 28-30; 34pp; German.
 XX
 CC The present Lactobacillus kefir alcohol dehydrogenase (ADH) was
 used in the isolation of a L. brevis ADH, which retains at least
 98% of its activity after 30 minutes at 20-60 degrees C and can be
 purified to a specific activity of at least 400 U/mg. The enzyme
 can be used to produce (R)-alcohols by enantioselective reduction
 of ketones of formula R1-CO-R2, where R1 and R2 = hydrogen (sic)
 or 1-20C alkyl, alkenyl, aryl or arylenyl (sic) optionally

CC substituted by halogen, NO2, OH or 1-20C alkoxy, "an optionally
 CC substituted 1-10C alkylene group, which is substituted by
 CC saturated, unsaturated or aromatic nitrogen, oxygen or sulphur
 CC heterocycles, or may be an optionally substituted polycoupled
 CC saturated and/or aromatic group" (sic) in the presence of the
 CC enzyme or cells containing it at 20-60 degrees C for 0.25-3 hours,
 CC or (S)-alcohols by incubating a racemic alcohol of formula
 CC R1-CHOH-R2 in the presence of the enzyme or cells containing it at
 CC 20-60 degrees C for 0.25-3 hours.
 XX
 SO Sequence 251 AA:
 Query Match 79.0%; Score 1019; DB 18; Length 251;
 Best Local Similarity 80.5%; Pred. No. 9, 3e-91;
 Matches 202; Conservative 14; Mismatches 35; Indels 0; Gaps 0;
 OY 2 SNRLDGKVALIINGGTGIGAIATPKFVEBGAQWITRHSVDGFRKAKSVGTPOIQFQ 61
 DB 1 TDRLKGKVALVGTGTGIGAIADKFEBAKAVITGRHADVGRKXXXXXXXXXXXXX 60
 OY 62 HDSSDEGWTKLDATEKAGPSTLVNNGIAVKNVSEETTAEMRKLAVNDGVFG 121
 DB 61 XXXXXXXXXXXXLPDATEARGPVTTVNNNGIAVKNVSEETTAEMRKLAVNDGVFG 120
 OY 122 TRIGIORMKNGIGASTINNSIEGFGDPSLGAVNASKAVRIMSAAIDCALKDQY 181
 DB 121 TRIGIAMKXXGIGASTINNSIEGFGDPTLGAVNASKAVRIMSAAIDCALKDQY 180
 OY 182 RVNTVHPGYTKTPLVDLPEAFEMSORTKPMCHIEPDIAICYLLNSKEKPTGS 241
 DB 181 RVNTVHPGYTKTPLVDLPEAFEMSORTKPMCHIEPDIAICYLLNSKEKPTGS 240
 OY 242 EFVVDGQYTAQ 252
 DB 241 EFVVDGQYTAQ 251
 RESULT 4
 AAB49773
 ID AAB49773 standard; protein; 254 AA.
 XX
 AC AAB49773;
 XX
 DT 23-APR-2001 (first entry)
 XX
 DE Protein with acetylpyridine derivative reducing action.
 XX
 KM Optically-active pyridineethanol derivative; asymmetric reduction.
 XX
 OS Candida maris.
 OS
 PN WO200105996-A1.
 XX
 PD 25-JAN-2001.
 XX
 PF 28-JUN-2000; 2000MO-JP04237.
 XX
 PR 21-JUL-1999; 99JP-0206503.
 XX
 PA (KANF) KANEKA CORP.
 XX
 PI Kawano S, Horikawa M, Yasohara Y, Hasegawa J;
 XX
 DR WPI; 2001-159546/16.
 DR N-PSDB; AAF29375, AAF29376.
 XX
 PT Efficient, high-yielding preparation of optically-active
 pyridineethanol derivatives by stereoselectively reducing
 acetylpyridine derivatives e.g. with enzyme having asymmetric reduction
 activity, for pharmaceutical intermediates -
 XX
 PS Claim 14; Fig 1; 76pp; Japanese.

CC This invention relates to a process for producing optically-active
 CC pyridineethanol derivatives by stereoselectively reducing acetylpyridine
 CC derivatives with an enzyme or enzyme source having asymmetric reduction
 CC activity. The process is efficient and high yielding to give R and S
 CC isomers by suitable manipulation. The method is for the preparation of
 CC optically-active pyridineethanol derivatives by stereoselectively
 CC reducing acetylpyridine derivatives, and also similarly for their
 CC polycyclic analogues, for use as pharmaceutical and agrochemical
 CC intermediates, as well as in fine chemical production. The present
 CC sequence represents the amino acid sequence of the enzyme used in the
 CC process which has acetylpyridine derivative reducing action.

CC Sequence 254 AA:

Query Match 35.3%; Score 456; DB 22; Length 254;
 Best Local Similarity 40.2%; Pred. No. 5e-36;
 Matches 104; Conservative 49; Mismatches 94; Indels 12; Gaps 5;

OY 1 MSNRIDGKVAITITGTLGIGLAATKFEVBEKAKVMTD-----RHSVGEKAKASVGT 54
 DB 1 MSYFNANKVLTGTLGIGLAATKFEVBEKAKVMTD-----RHSVGEKAKASVGT 60
 OY 55 DOIQFQHDSDSDGWTKLFPDATEKAFGVSTLVNNAIGAVNKSVEETTAEMRKLAVN 114
 DB 61 N-VQYIADASKADENKELISLTSFGLDYVCANAGIATFTQTTDISTVWRKVTISN 119
 OY 115 LDGVFFGRGLGIQRKKNKGASIIINSSIEGFGVDPGLGAVNASKGAVRIMSKSALDC 174
 DB 120 LDGVFMELKLAQVFLSKNPGAIYVMSIHSYVAFGLSHGCAANGKGLKLTQTALEY 179
 OY 175 ALKDYVRNTHPGYIKTPLVDDLPGAEEAMSQR-TKTPMGHIGEPNDIATVICYLASN 233
 DB 180 AAK--GIRVNSVNPYIKTPLDICP--KEHMDVLTQHPHIGLRPEETASAVAFICSD 235
 OY 234 ESKFATGSEFVVDGYYTAQ 252
 DB 236 EATFINGISLVPDGGYTA 254

RESULT 5

AAB47522 standard; Protein: 254 AA.

AC AAB47522;

DT 04-DEC-2001 (first entry)

DE (R)-2-octanol dehydrogenase.

KM (R)-2-octanol dehydrogenase; ketone; alcohol; beta-NAD; co-enzyme;
 KM oxidize; optical isomer; (R)-2-octanol; 4-haloacetate ester;
 KM (S)-4-halo-3-hydroxybutyrate ester; HMG-CoA reductase inhibitor;
 KM D-carnitine; (R)-propoxybenzene.

OS Pichia finlandica.

PN M0200161014-A1.

PD 23-AUG-2001.

PF 15-FEB-2001; 2001MO-JF01082.

PR 16-FEB-2000; 2000JP-0043506.

PR 08-DEC-2000; 2000JP-0374593.

PA (DAIL) DAICEL CHEM IND LTD.

PI Kudoh M, Yamamoto H;

DR WPI: 2001-596701/67.

DR N-PSDB; AAH43472.

PT (R)-2-octanol dehydrogenase for producing intermediates for HMG-CoA

PT reductase inhibitors or D-carnitine
 XX Claim 9; Page 83-85; 97pp; Japanese.

PS This sequence represents (R)-2-octanol dehydrogenase which has the
 XX following characteristics:
 CC (1) produces ketones by oxidizing alcohol using beta-NAD as a
 CC co-enzyme; and produces alcohols by reducing ketones using beta-NADH
 CC as a co-enzyme; and
 CC (2) preferentially oxidizes the optical isomer (R)-2-octanol; and
 CC reduces 4-haloacetate ester to produce (S)-4-halo-3-
 CC hydroxybutyrate ester.
 CC (S)-4-halo-3-hydroxybutyrate esters are useful as intermediates
 CC for HMG-CoA reductase inhibitors or D-carnitine. (R)-propoxybenzene
 CC derivatives are particularly useful as intermediates for optical
 CC isomers of olofoxane (S)-(-)-9-fluoro-3-methyl-10-(4-methyl-1-
 CC piperazinyl)-7-oxo-2,3-dihydro-7H-pyrido(1,2,3-de)(1,4) benzoxadiazin-
 CC 6-carboxylic acid).

CC Sequence 254 AA:

Query Match 34.9%; Score 450; DB 22; Length 254;
 Best Local Similarity 39.0%; Pred. No. 1.9e-35;
 Matches 101; Conservative 46; Mismatches 100; Indels 12; Gaps 5;

OY 1 MSNRIDGKVAITITGTLGIGLAATKFEVBEKAKVMTD-----RHSVGEKAKASVGT 54
 DB 1 MSYFNANKVAVTALSLGIGLAATKFEVBEKAKVMTD-----RHSVGEKAKASVGT 59
 OY 55 DOIQFQHDSDSDGWTKLFPDATEKAFGVSTLVNNAIGAVNKSVEETTAEMRKLAVN 114
 DB 60 DNHYVQADSKEDDNKKLSETLATFGGLDYVCANAGIATFTQTTDISTVWRKVTISN 119
 OY 115 LDGVFFGRGLGIQRKKNKGASIIINSSIEGFGVDPGLGAVNASKGAVRIMSKSALDC 174
 DB 120 LNVGYLLDKLAINYMLKSKPGVIVNMGSVHFAAPGLAHYGAAGGVKLLTQTALEY 179
 OY 175 ALKDYVRNTHPGYIKTPLVDDLPGAEEAMSQR-TKTPMGHIGEPNDIATVICYLASN 233
 DB 180 A--SHGIRVNSVNPYIKTPLDICP--KERLDKLVSLHPHIGLRPEEVADAVAFICSD 235
 OY 234 ESKFATGSEFVVDGYYTAQ 252
 DB 236 EATFINGVSLVPDGGYTAQ 254

RESULT 6

AA556815 standard; Protein: 258 AA.

AC AA556815;

DT 31-MAR-2000 (first entry)

DE Bacillus D-arabinitol dehydrogenase.

KM D-arabinitol dehydrogenase; clinical diagnosis; mycosis.

OS Bacillus sp.

PN JP11332569-A.

PD 07-DEC-1999.

PF 26-MAY-1998; 98JP-0143637.

PR 26-MAY-1998; 98JP-0143637.

PA (IKED-) IKEDA SHOKKEN KK.

PA (NIPK) NIPPON KAYAKU KK.

DR WPI: 2000-091353/08.

DR N-PSDB; AAZ46762, AAZ46763.

XX Arabinitol dehydrogenase gene encoding D-arabinitol dehydrogenase -
 PT useful as a clinical diagnosing agent for mycosis
 XX
 PS Claim 1: Page 10-11, 14pp: Japanese.
 CC The invention relates to gene encoding D-arabinitol dehydrogenase,
 CC isolated from *Bacillus* sp. 1KD-3A868 strain. The protein can be expressed
 CC by standard recombinant methodologies. D-arabinitol dehydrogenase is used
 CC as a clinical diagnosing agent for mycosis. The present sequence
 CC represents the D-arabinitol dehydrogenase enzyme.
 XX
 SQ Sequence 258 AA:
 Query Match 31.0%; Score 400; DB 21; Length 258;
 Best Local Similarity 39.4%; Pred. No. 1.4e-30;
 Matches 100; Conservative 41; Mismatches 101; Indels 12; Gaps 7;
 OY 4 RLDGKVAITIGTGIGLATAITKFEVSGAKVMTDRHSVDGEKAA--KSVGTPDQIOFF 60
 DB 8 RLDGKVAITIGTGIGLATAITKFEVSGAKVMTDRHSVDGEKAA--KSVGTPDQIOFF 65
 OY 61 QHDSDEGWTKLFDATERKAFGPVSTLVNNAIGAVNKSVEETTTAEMRKILAVNLGVFF 120
 DB 66 QTDVTDAAQVEALIRQVEBOYGRLDVLYNNAGIVHKDRAEELPYETNNRVNVLNSVFL 125
 OY 121 GTRLGIDRMKNKGASIIINMSISIEG-FVGDPS-LGAVNASKGAVRINKSAALDCALKD 178
 DB 126 MSKAGKVMIRQKG-SIINISSMSGLIVNTPQQAAYNVSKAGVIMLTSLASEMA--P 182
 OY 179 YDPAVNTVHHGVIKTPLVDD--LPGAEAMSQRKTPMGHIGEPNDIAYICVYLASNEK 236
 DB 183 HGRAVNTIAPGMYKTKLTERYFAAGGEMIDKMLMTMGRGVPHELGIAVYLASDASS 242
 OY 237 FATGSEFVVDGYYT 250
 DB 243 FATGCVFTIDGYYT 256
 RESULT 7
 ID ABP38717 standard; Protein; 257 AA.
 XX
 AC ABP38717;
 DT 24-JUL-2002 (first entry)
 XX
 DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3562.
 XX
 KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
 KW antibacterial; gene therapy.
 XX
 OS Staphylococcus epidermidis.
 XX
 PN US6380370-B1.
 PD 30-APR-2002.
 PF 13-AUG-1998; 98US-0134001.
 PR 14-AUG-1997; 97US-055779P.
 PR 08-NOV-1997; 97US-064964P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 PI Doucette-Stamm LA, Bush D;
 DR WPI: 2002-381255/41.
 DR N-PDB; ABN91262.
 XX
 PT Novel isolated nucleic acid encoding a staphylococcus epidermidis
 PT polypeptide, useful for diagnosing and treating bacterial infections -
 XX

PS Disclosure; SEQ ID 3562; 267pp; English.
 XX
 CC ABN90538 to ABN93374 represent *Staphylococcus epidermidis* open reading
 CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
 CC given in ABP5124 to ABP37960. The *S. epidermidis* sequences have
 CC antibacterial activity and can be used in gene therapy. The sequences
 CC can also be used in the diagnosis and treatment of bacterial infections,
 CC particularly *S. epidermidis* infections. The sequences can be used to
 CC screen for compounds able to interfere with the *S. epidermidis* life
 CC cycle or inhibit *S. epidermidis* infection.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC USPTO web site.
 XX
 SQ Sequence 257 AA:
 Query Match 29.1%; Score 376; DB 23; Length 257;
 Best Local Similarity 33.7%; Pred. No. 3e-28;
 Matches 86; Conservative 59; Mismatches 94; Indels 16; Gaps 6;
 OY 4 RLDGKVAITIGTGIGLATAITKFEVSGAKVMTDRHSVDGEKAAKSVGTPDQIO--FFQ 61
 DB 11 KLTGKVAIVIGAGGIGAGGAGMAEALAQAGANIVADLSNIGETRTITSTGCVKTSLK 70
 OY 62 HDSDEGWTKLFDATERKAFGPVSTLVNNAIGAVNKSVEETTTAEMRKILAVNLGVFF 121
 DB 71 LDITHLEVDNIDVYVREYKIDILVNNASISIODTENISYEEMLEKIMLSNGAFSV 130
 OY 122 TRLGIDRMKNKGASIIINMSISIEGFVDPS--LGAVNASKGAVRINKSAALDCALKDY 179
 DB 131 AQTGROMIERKQSG-SMINSSVGLLANKTODDSVETSKAGVTMLTSLAREMS--RY 187
 OY 180 DVAVNTVHHGVIKTPLVDD--LPGAEAMSQRKTPMGHIGEPNDIAYICVYLASNEK 236
 DB 188 GIXVNAIAPGYMT-----IETEKILNDNTETMTTHERGERGEBELAGIIVYLASDASS 241
 OY 237 FATGSEFVVDGYYT 251
 DB 242 FTGGSVFNIDGYSY 256
 RESULT 8
 ID AAU37095 standard; Protein; 272 AA.
 XX
 AC AAU37095;
 DT 14-FEB-2002 (first entry)
 XX
 DE Staphylococcus aureus cellular proliferation protein #1265.
 XX
 KW Antisense: prokaryotic cellular proliferation protein;
 KW antibiotic; antibacterial; drug design.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO200170955-A2.
 PD 27-SEP-2001.
 PF 21-MAR-2001; 2001WO-US09180.
 PR 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253623P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 XX

PI Yamamoto RT, Xu HH;
 XX WPI: 2001-611495/70.
 DR N-PSDB: AAS54954.
 XX
 XX New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX
 PS Example 3: Seq ID No 12688; 511pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
 CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 272 AA:

Query Match 28.6%; Score 369; DB 22; Length 272;
 Best Local Similarity 35.8%; Pred. No. 1.6e-27;
 Matches 92; Conservative 42; Mismatches 109; Indels 14; Gaps 6;

QY 4 RUDGVAITGTGIGLAIATKFEVGAQVMITDRHSDGKAKSVGTPOIOFQHD 63
 DB 3 RLENVAVATGASTGIGQSAIALDQAGAVLVADIAEAVSEYDKTKSKGAKAYVD 62
 QY 64 SDEGKTKLEPATEKAFSPVSTLVNNAI--AVNKSVEETTAEMKRLAVNLDGVFFG 121
 DB 63 IASEQOINDFASEIEQFGHVDVLFNNAGVDNAAGR-IHEYPDVYDKIMNVDMRGFTLM 121
 QY 122 TRLGQRKKNKGLASITMSIEGFVGPDSLGAYNASKAVRIMSKSALDKLDYDV 181
 DB 122 TKMLPLMAMTK--GGSIVNTSSFGQAADLYRSGYNAAKGAIVNFTKSIIEYG-RD-GI 177
 QY 182 RVNTVHPGYIKTPLVDLPGAE-----AMSOPTKTPMGHIGEPNDIAVICYLLASNE 234
 DB 178 RANAIAPGTIERPLVDKLTGISEDKGAFAREOKMWTPLGRIGKEPVGLVFLASDE 237
 QY 235 SKPATGSEFVVDGGYTA 251
 DB 238 SSFTIGETIRIDGGYMA 254

RESULT 9
 ABB54214
 ID ABB54214 standard; Protein: 253 AA.
 AC ABB54214;
 DT 16-MAY-2002 (first entry)
 DE Lactococcus lactis protein buta.
 XX Lactococcus lactis protein buta.
 XX Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
 OS Lactococcus lactis IL1403.
 XX
 XX FR2807446-A1.
 XX
 XX

PD 12-OCT-2001.
 XX
 PF 11-APR-2000; 2000FR-0004630.
 XX
 PR 11-APR-2000; 2000FR-0004630.
 XX
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 XX
 XX Bolotine A, Sorokine A, Renault P, Ehrlich SD;
 XX WPI: 2002-043418/06.
 DR
 XX
 PT New nucleotide sequence useful in the identification of Lactococcus
 PT lactis and related species -
 XX
 PS Claim 6: SEQ ID No 916; 2504pp; French.

CC The present invention is related to a Lactococcus lactis nucleotide
 CC sequence (ABA90521) and related proteins (ABB53300-ABB55621). The
 CC nucleic acid sequence is useful in the detection and/or amplification of
 CC nucleic acid sequence, particularly to identify Lactococcus lactis or
 CC related species. The proteins of the invention are useful for the
 CC biosynthesis or biodegradation of a composition of interest. The
 CC invention helps research in lactic bacteria, particularly useful in the
 CC production of yogurt and cheese.
 CC Note: The sequence data for this patent is based on equivalent patent
 CC WO200177334 (published 18-OCT-2001) which is available in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 253 AA:

Query Match 28.5%; Score 368; DB 23; Length 253;
 Best Local Similarity 34.3%; Pred. No. 1.8e-27;
 Matches 86; Conservative 48; Mismatches 103; Indels 14; Gaps 4;

QY 8 KVAITGTGIGLAIATKFEVGAQVMITDRHSDGKAKSVGTPOIOFQHDSSDE 67
 DB 3 KIAAAYGAGGIGFALAKRLYNDFKVAIIDYNETAQAKKEIG--ENSFAIKADYSR 60
 QY 68 DQWTKLFDAEKAFSPVSTLVNNAI--AVNKSVEETTAEMKRLAVNLDGVFFGRLGIQ 127
 DB 61 EOYISLNAVDFGDLNVAANNAGIAPPTQIETITPEQFHOVYININVGVLMTGTOTSTA 120
 QY 128 RKNKGLASITMSIEGFVGPDSLGAYNASKAVRIMSKSALDKLDYDVAVNTVH 187
 DB 121 LFRKLGHGKIINATQAGVGNPNMLYSSSKRAVAGMTQIARD--LAEGITVNAVA 178
 QY 188 PCYIKTPLVDL-----PGAEANSSQRT--KTPMGHIGEPNDIAVICYLLASNESEKF 237
 DB 179 PCIVKTPMFMFDIAHQVKNAGKDDQMGTFAKDIAKRLSEPEDVANVSEFLAGPSNY 238
 QY 238 ATGSEFVVDGG 248
 DB 239 ITGQTIIVDGG 249

RESULT 10
 AAR27757
 ID AAR27757 standard; Protein: 261 AA.
 AC AAR27757;
 DT 11-MAR-1993 (first entry)
 DE Glucose dehydrogenase.
 XX GDH; mutant; recombinant; mass production; tetramer; thermostable.
 XX Bacillus megaterium.
 OS
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 96
 FT /note= "site of Glu->Val or Lys mutation"

FT Misc-difference 252 /note- "site of Gln->Leu mutation"
 FT Misc-difference 253 /note- "site of Tyr->Glu mutation"
 FT Misc-difference 22 /label- Ser, Ala
 FT Misc-difference 43 /label- Asp, Glu
 FT Misc-difference 79 /label- Ala, Ser
 FT Misc-difference 95 /label- Leu, Met
 PN JP04258293-A.
 XX 14-SEP-1992.
 XX 13-FEB-1991: 91JP-0106927.
 XX 13-FEB-1991: 91JP-0106927.
 XX (AMAN) AMANO PHARM KK.
 XX WPI: 1992-354684/43.
 DR Glucose dehydrogenase prep. using transformed recombinant DNA
 PT from *Bacillus megaterium* - has specified transformations giving
 PT glucose dehydrogenase-expressing vector, introduced into *E. coli*.
 PT for culture
 XX
 XX Claim 1: Page 8; 12pp: Japanese.
 CC The glucose dehydrogenase enzyme is encoded by a recombinant DNA
 CC clone from *Bacillus megaterium*. The DNA sequence may be mutated by
 CC site directed mutagenesis to introduce mutations to the protein
 CC sequence (see feature table). The DNA may be used to transform *E.*
 CC *coli* cells, and transformants may be cultured to mass produce GDH.
 CC The mutant GDH is not influenced by ion strength, exists as a
 CC tetramer and is thermostable.
 XX
 XX Sequence 261 AA:
 SQ
 Query Match 28.5%; Score 367.5; DB 13; Length 261;
 Best Local Similarity 33.3%; Pred. No. 2.1e-27;
 Matches 85; Conservative 49; Mismatches 112; Indels 9; Gaps 4;
 OY 1 MSNRDGVKVAITGGTGLGIAIAATKFEVEGAKVMTDRHSDVGEKAA---KSVGTPDQ 56
 DB 1 MYKDLGGKVVVITGSSGLGKXMAIRATEKAKVYVVRKSEKXANVLEIKKVG--GE 58
 OY 57 IOFFQHDSSDEDCWTKLFDATERKAFGVSSTLVNNAIAVNSVEETTTAEMRKLLAVNLD 116
 DB 59 AIAVKGQVTVESDVINLVOSXIKFEGKLDVMINNAGXENPVSSHEMSLSDNNKXIDTNLT 118
 OY 117 GFVEGTGLGIORMKNGKLGASINSSIEGFGDPSSGAVYNSGAVRMSKSAALCAL 176
 DB 119 GAFGSEAKIKFVENDIKGTIVIMSSVHEKIPPLVHTAASGKMLMETLALLETAP 178
 OY 177 KDVDVAVNTHPGYIKPL-VDDLPAGEAMSOFTKTPMGHIGSPNDIAYICVLIASNES 235
 DB 179 K--GIRVNNIGPAINPPIINAEKFADEQRAVDSEMI PMGTIGPEELIAAANAALASSE 236
 OY 236 KFAATSEFVVDGCT 250
 DB 237 SYVTGTLFADGGMT 251

DT 18-JUN-2002 (first entry)
 XX Lactobacillus rhamnosus acetoin dehydrogenase butA.
 DE
 XX Enzyme: flavour; aroma; texture; nutritional; dairy manufacture; therapy;
 KW fermentation process; anti-infection; rotavirus infection; heart disease;
 KW infantile diarrhoea; lactose digestion; anti-cancer; autoimmune disorder;
 KW anti-mutagenesis; immune system modulation; allergy; *Helicobacter pylori*;
 KW antihypertensive effect; urogenital infection; hepatic encephalopathy;
 KW bowel syndrome; endocarditis; transgenic microbe; acetoin dehydrogenase;
 KW butA; EC 1.1.1.5.
 XX
 XX Lactobacillus rhamnosus HN001.
 OS
 XX WO200212506-A1.
 PN
 XX 14-FEB-2002.
 PD
 XX 08-AUG-2001; 2001WO-N200160.
 PF
 XX 08-AUG-2000; 2000US-0634238.
 XX 28-NOV-2000; 2000US-0724623.
 PR
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 PA (VIAL-) VIALACTIA BIOSCIENCE NZ LTD.
 XX Glenn M, Havukkala ID, Bloksberg LN, Lubbers MW, Dekker J;
 PI Christenson AC, Holland R, O'toole PM, Reid JR, Coolbear T;
 XX
 XX WPI: 2002-241760/29.
 DR N-PSDB; AAD31886.
 DR
 XX New polynucleotides and polypeptides from *Lactobacillus rhamnosus*,
 PT useful in e.g. improving the flavor, aroma, texture and health-related
 PT benefits of milk-derived products, or in increasing properties of
 PT microbes -
 XX
 PS Claim 11: Fig 50; 257pp: English.
 XX
 CC The present invention relates to a new isolated polynucleotide comprising
 CC a sequence present in *Lactobacillus rhamnosus* strain HN001 and encoding a
 CC polypeptide capable of modifying the flavour, aroma, texture, nutritional
 CC and health benefits of milk-derived products, and/or survivability of
 CC microbes in dairy manufacturing processes. The polynucleotides are useful
 CC for improving the properties of microbes used in the manufacture of milk-
 CC derived products such as cheeses, yogurt, fermented milk products, sour
 CC milks and buttermilk; in modifying the flavour, aroma, texture and health-
 CC related benefits of milk-derived products and in increasing the survival
 CC of microbes during industrial fermentation processes. The bacteria may be
 CC used to increase resistance to enteric pathogens and anti-infection
 CC activity, including treatment of rotavirus infection and infantile
 CC diarrhoea; aid in lactose digestion; as anti-cancer and anti-mutagensis;
 CC liver cancer reduction; reduction of small bowel bacterial overgrowth;
 CC immune system modulation and treatment of autoimmune disorders and
 CC allergies; treatment of allergic responses to foods; reduction of blood
 CC lipids and prevention of heart disease; antihypertensive effect;
 CC prevention and treatment of urogenital infections, *Helicobacter pylori*,
 CC or hepatic encephalopathy; treatment of inflammatory bowel disorder and
 CC irritable bowel syndrome; modulation of endocarditis; and for improved
 CC protein and carbohydrate utilization and conversion. The transgenic
 CC microbial population can be administered to a mammal as an anti-
 CC carcinogenic agent. The present sequence is *Lactobacillus rhamnosus*
 CC acetoin dehydrogenase butA. The EC number for acetoin dehydrogenase is
 CC 1.1.1.5.
 XX
 XX Sequence 261 AA:
 SQ
 Query Match 28.4%; Score 366.5; DB 23; Length 261;
 Best Local Similarity 33.5%; Pred. No. 2.0e-27;
 Matches 85; Conservative 50; Mismatches 112; Indels 7; Gaps 4;
 OY 1 MSNRDGVKVAITGGTGLGIAIAATKFEVEGAKVMTDRHSDVGEKAAASVGTPOIO 58

Db 1 MYRDLNGKAVVYTGSGKIGAGIAERFGDEHMAVINYIADGHEGARKTADTIRKNGQAV 60
 QY 59 FFOHDSDEDCGKTLKEDATEKAFGPVSTLVNNGIAVNSVEETTTAEMKLLAVNDGV 118
 Db 61 SIHADVSTEGIASIVKTAESEFGRDVMVNNAGMEIKAPTHEVSLDDMKVIAINOTGV 120
 QY 119 FFGTRLGIGQRMKNKLGASIIINMSIEGVPDPSLGAYNASKGAVRIMSKSALDCAKD 178
 Db 121 FLGARAAIATFLDHHQPGKITINISSVHEQIPWPTFASVAAAKGSVKLFTETIAMEYA--N 178
 QY 179 YDVRVNTVHPGYIKTPLYVDLPGAEAMSOPT--KTPMCHIGEPRNDIAYICVYLAESK 236
 Db 179 RGIRVNAIGAPAEIETP--INAEKFAADKAOYDQIVAMIPQGRILKEPEVAAAGAMWLASTE 237
 QY 237 FATGSEFVVDGCT 250
 Db 238 YVTGTITLFDGCMT 251

RESULT 12

AAR04044
 ID AAR04044 standard; protein: 261 AA.

AC AAR04044;
 DT 02-MAR-1993 (first entry)
 DE Glucose dehydrogenase.
 KM GDH; vector; E. coli; enzyme; assay; food.
 OS Bacillus megaterium.

EH Key Location/Qualifiers
 FT Misc-difference 22
 FT /label= SER, Ala
 FT Misc-difference 43
 FT /label= ASP, Glu
 FT Misc-difference 79
 FT /label= ALA, Ser
 FT Misc-difference 95
 FT /label= LEU, Met

JP02072878-A.

PD 13-MAR-1990.

PF 06-SEP-1988; 88JP-0223343.

PR 06-SEP-1988; 88JP-0223343.

PA (AMANO) AMANO PHARM KK.

DR WPI; 1990-121044/16.

PT Glucose dehydrogenase prodn. from Bacillus megaterium - by
 PT culturing recombinant DNA-contg. transformants in nutrient
 PT culture medium, used in food industry

PS Claim 1; 12pp; Japanese.

CC DNA encoding glucose dehydrogenase (GDH) derived from B. megaterium
 CC encodes the amino acid sequence below. The DNA may be integrated
 CC into a vector for replication in E. coli. A large amt. of GDH may
 CC be produced at low cost. The GDH is used in clinical laboratory
 CC tests in the food industry in enzymic assays for glucose
 CC determination.

XX Sequence 261 AA;

Query Match 28.3%; Score 364.5; DB 11; Length 261;
 Best Local Similarity 33.3%; Pred. No. 4, 1e-27;
 Matches 85; Conservative 49; Mismatches 112; Indels 9; Gaps 4;

QY 1 MSNRDLGKVAITTGCTLGIGLAATKFEVGAQWITDHRSDVGERAA----KSVGTPDQ 56
 Db 1 MKRDLGKVVVITGSGTGKXMAIRFATEKAKVVVNYRSKEXEANSVLEIKVQ--GE 58
 QY 57 IOFQHDSDEDCGKTLKEDATEKAFGPVSTLVNNGIAVNSVEETTTAEMKLLAVND 116
 Db 59 AIAVAGDVTSVDVNLVQSAIKERKGLDVMINMGXENPVSSHEMSLSDMKVITDNL 118
 QY 117 GVFETRLGIGQRMKNKLGASIIINMSIEGVPDPSLGAYNASKGAVRIMSKSALDCA 176
 Db 119 GAFUGSREAIKIFYENDIKGTVINMSVHEKIPMPLFVHYAASKGKMLTETIALEYAP 178
 QY 177 KDVVRVNTVHPGYIKTPLYVDLPGAEAMSOPT--KTPMCHIGEPRNDIAYICVYLA 235
 Db 179 K--GIRVANNIGPGLINTINAEKFAPOPRADVESMIPMGYIGPEEIAVAAMWLASTE 236
 QY 236 KEATGSEFVVDGCT 250
 Db 237 SYVTGITLFDGCMT 251

RESULT 13

AAR24018
 ID AAR24018 standard; protein: 261 AA.

AC AAR24018;

DT 27-NOV-1992 (first entry)

DE Thermostable glucose dehydrogenase from Bacillus megaterium.
 DE Thermostable; increased heat stability; GDH.

OS Bacillus megaterium.

EH Key Location/Qualifiers
 FT Misc-difference 22
 FT /label= Ser, Ala
 FT Misc-difference 43
 FT /label= ASP, Glu
 FT Misc-difference 79
 FT /label= ALA, Ser
 FT Misc-difference 95
 FT /label= LEU, Met

FT Misc-difference 96

FT /note- "together with residues 252,253 may be
 FT replaced by a thermostability-conferring
 FT amino acid provided that taken together
 FT they are not Glu, Gln, and Tyr respectively"

FT Misc-difference 252

FT /note- "together with residues 96,253 may be
 FT replaced by a thermostability-conferring
 FT amino acid provided that taken together
 FT they are not Glu, Gln, and Tyr respectively"

FT Misc-difference 253

FT /note- "together with residues 96,253 may be
 FT replaced by a thermostability-conferring
 FT amino acid provided that taken together
 FT they are not Glu, Gln, and Tyr respectively"

XX US114853-A.

XX 19-MAY-1992.

XX 22-SEP-1989; 89US-0410844.

XX 22-SEP-1988; 88JP-0237699.

XX (AMANO) AMANO PHARM KK.

XX Makino Y, Negoro S, Okada H, Urabe I;

DR WPI: 1992-192176/23.

XX DNA contg. glucose dehydrogenase gene of *Bacillus megaterium*.

PT used to express heat stable protein in *Escherichia coli*, e.g. with

PT glutamine 96 replaced by alanine

XX

PS Claim 1; Column 13; 10pp; English.

XX

CC A DNA library was prepared in *E. coli* C600, and screened with probe

CC AA029704, resulting in 3 positive colonies. These were cultured, and

CC plasmid DNA prepared from them and cut with EcoRI and SalI. The

CC probe AA029704 was then used to probe a PAGE gel and found to

CC strongly hybridise with a 3.6kb fragment. The 3 colonies were all

CC thus found to have the same plasmid, and this was named pGD1. pGD1

CC was cut with EcoRI and Sau3AI, and a 930bp fragment produced and

CC sequenced, and was found to encode the sequence given. pGD1 was

CC then cut with EcoRI and PvuII and a 1.5kb fragment isolated. This

CC was then cloned into expression vector pKR223-3 and transformed into

CC *E. coli* JM105.

XX

SQ Sequence 261 AA;

Query Match 28.3%; Score 364.5; DB 13; Length 261;

Best Local Similarity 33.3%; Pred. No. 4.1e-27;

Matches 85; Conservative 49; Mismatches 112; Indels 9; Gaps 4;

OY 1 MSNRDLGKVALITGGTGLGIAIAIKFEVEGAKVMTDRHSDVGEKAA---KSVGTPDQ 56

1 MYKDLKGVVVTSSSTGLGKXMAIRFATERAKAVVNVYRSKEXANSVLEIEIKVGG--GE 58

DB

OY 57 IQFQHDSDDEGWTKEFDEAKAFGPYSTLVNNAAGVNVKSVETTTAEKRKLAVLD 116

59 AIAVKGQVTVESDVIVLVQSKIKFEKGLDVIMINNAKXNPVSSHMSLSDNKKVYIDTMLT 118

DB

OY 117 GVEFGTRIGIORMNKKGLGASIIINNSIEGFVGPDSLCAYVNAKCAVRIMSKAALDQAL 176

119 GAFIISREAIKFEVENDIKGVINNSVHEKIPMPLFHYVYASKGMKIMETTLALEYAP 178

DB

OY 177 KDVIVRVNVTVPYGIKTPPL-VDDLPGAEANSSQRTKTPMGHIGEPNDIAYICVYLANS 235

179 K--GIRVNNIGPCAINTPINAEKFPADPOERADVESMIPMGYIGEPBEIAVAAMLASSEA 236

DB

OY 236 KFAFGSEFVVDGGYT 250

237 SYVTGITLFPADGGMT 251

DB

RESULT 14

AAU34193

ID AAU34193 standard; Protein: 251 AA.

XX

AC AAU34193;

XX

DT 14-FEB-2002 (first entry)

XX

DE Staphylococcus aureus cellular proliferation protein #469.

XX

KW Antisense: prokaryotic cellular proliferation protein;

KW antibiotic; antibacterial; drug design.

XX

OS Staphylococcus aureus.

XX

PN MO200170955-A2.

PD

XX 27-SEP-2001.

PF

XX 21-MAR-2001; 2001MO-US09180.

XX

PR 21-MAR-2000; 2000US-191078P.

PR 23-MAY-2000; 2000US-206848P.

PR 26-MAY-2000; 2000US-207727P.

PR 23-OCT-2000; 2000US-242578P.

PR 27-NOV-2000; 2000US-253625P.

XX

PR 22-DEC-2000; 2000US-257931P.

PR 16-FEB-2001; 2001US-269308P.

XX

PA (ELIT-) ELITRA PHARM INC.

XX

PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr CJ;

PI Yamamoto RT, Xu HH;

XX

DR WPI: 2001-611495/70.

XX

DR N-PSDB: AAS52052.

XX

PT New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids.

XX

PS Example 3; Seq ID No 5689; 51pp; English.

XX

CC The invention relates to antisense inhibitors of genes essential to

CC prokaryotic cellular proliferation, their use in identifying the

CC genes, their use in the discovery of novel antibiotics, the essential

CC genes themselves and the encoded proteins. The prokaryotes used are

CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*

CC pneumoniae, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The

CC invention is also useful for the identification of potential new targets

CC for antibiotic development. The antisense nucleic acids can also be used

CC to identify proteins used in proliferation, to express these proteins,

CC and to obtain antibodies capable of binding to the expressed proteins.

CC The proteins can be used to screen compounds in rational drug discovery

CC programmes. The antisense nucleic acid sequence is also useful to screen

CC for homologous nucleic acids which are required for cell proliferation in

CC a wide variety of organisms. The present sequence represents an

CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic

CC format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 251 AA;

Query Match 28.2%; Score 364; DB 22; Length 251;

Best Local Similarity 35.5%; Pred. No. 4.3e-27;

Matches 91; Conservative 42; Mismatches 109; Indels 14; Gaps 6;

OY 5 LDGKVALITGGTGLGIAIAIKFEVEGAKVMTDRHSDVGEKAAKSVGTPDQIOFFQDS 64

1 LENKVAVVTGASTGIGASAIALAQEGAYVLAVDAEAVSEVVDKIKNSGKAKAYVVDI 60

DB

OY 65 SDEGWTLPATEKAFGPYSTLVNNAAGI--AVNKSVETTTAEKRKLAVNLQVFEFGT 122

61 ASEDQIDNFASEIRFOFHVVLVFNMGVDNAAGR-IHEYPTDYVDKIMNMDMGTFIMT 119

DB

OY 123 RLGIORMNKKGLGASIIINNSIEGFVGPDSLCAYVNAKCAVRIMSKAALDQALQDVYR 182

120 KMLPLAMTK--GGSIVTSSFSQCADLYRSGVNAAGAVINFTKSAITEG-RD-GIR 175

DB

OY 183 VNTVHPGYIKTPVDDLPGABE-----ANSORTKTPMGHIGEPNDIAYICVYLANS 235

176 ANAIAFGTIEPVLVDKLTGTSDEKKAFRBNQWMPFLGIGPBEVGLVVFASDES 235

DB

OY 236 KFAFGSEFVVDGGYT 251

236 SFITGETIRIDGVA 251

DB

RESULT 15

AA010740

ID AA010740 standard; Protein: 272 AA.

XX

AC AA010740;

XX

DT 26-JAN-2001 (first entry)

XX

DE *B. megaterium* glucose dehydrogenase GLGDH protein.

XX

Glucose dehydrogenase; GlcDH; fusion protein; detection.

Bacillus megaterium.

MO200049039-A2.

24-AUG-2000.

08-FEB-2000; 2000MO-EP00978.

19-FEB-1999; 99DE-1006920.

(MERE) MERCK PATENT GMBH.

Linxweller W, Burger C, Poeschke O, Hofmann U, Wolf A.

WPI; 2000-558290/51.

N-PSDB; AAA97948.

Glucose dehydrogenase, fusion proteins, useful in expression systems for quick detection of foreign proteins by gel electrophoresis -

Disclosure; Page 54-55; 63pp; German.

This invention describes a novel recombinant fusion protein (A) comprising at least a first and a second amino acid sequence, characterized in that the first sequence has the biological activity of a glucose dehydrogenase. Glucose dehydrogenase is useful as a detector protein (in a detection system) for any type of recombinant protein/polypeptide in a fusion protein. Glucose dehydrogenase can be used to detect protein-protein interactions, where it corresponds to a partner of a recombinant protein/polypeptide. Expression vectors encoding the fusion proteins are useful to optimize the expression of the recombinant protein/polypeptide in a recombinant production method. The host cell is also useful for recombinant production of the protein/polypeptide. The fusion proteins containing glucose dehydrogenase can be quickly detected in SDS-PAGE gels. This sequence represents the Bacillus megaterium glucose dehydrogenase, GlcDH which is used in the construction of fusion proteins as described in the method of the invention.

Sequence 272 AA;

Query Match 28.28; Score 363.5; DB 21; Length 272;

Best Local Similarity 31.5%; Pred. No. 5.4e-27; Mismatches 82; Conservative 51; Indels 19; Gaps 4;

1 MSNRLDGKVAIIITGGTIGIGLAATKFEVEGAKYMIT-----DRHSDVGEKAQSV 51
1 MYTDLADKVVYITGGTIGIGLAATKFEVEGAKYMIT-----DRHSDVGEKAQSV 51
52 GTPDQIQFQHDSSDEDEGWTKLEDATEKAFGPVSTLVNAGIAVNSVEETTAEMRKL 111
61 -----IYGGDVTKBEDVYVNLVOTAIKEFTLDMINAGVENPVSHSLSDMNKVI 113
112 AVNLDGVFEFTGIGIQAKKKGAGASTIINSSIGCEVGPDSLGAVNASKGAVRINSKSA 171
114 DTNLTCGAFGLSREAIKVFYENDIKGVINNSVHEMIPWLFVHYASKGKMLMETLA 173
172 LDCALKDQVRYVNTVHPGYKTPLE-VDDLPGAEEAMSGRTKTPMGHIGEPNDIAICYIL 230
174 LEYAKR--GIRVNNIGGAMNPINNEKFADEPGRADVESMIPMGYICKPREVAVAFL 231
231 ASNESKFAATGSEFVVDGTY 250
232 ASSQASVYTGITLFAADGWT 251

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 17:14:51 ; Search time 14 Seconds

(Without alignments)
529.613 Million cell updates/sec

Title: US-09-910-033A-2

Perfect score: 1290
Sequence: 1 MSNRDGVKVAIIITGTTGIC.....NESKFRGSEFVVDGCTRAQ 252

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep: *
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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1277	99.0	252	3	US-08-822-322-8	Sequence 8, Appl1
2	1277	99.0	252	4	US-09-466-109-8	Sequence 8, Appl1
3	1019	79.0	251	3	US-08-822-322-9	Sequence 9, Appl1
4	1019	79.0	251	4	US-09-466-109-9	Sequence 9, Appl1
5	407.5	31.6	255	4	US-08-815-225-4	Sequence 4, Appl1
6	395.5	30.7	256	4	US-09-504-358-14	Sequence 14, Appl1
7	395.5	30.7	256	4	US-09-954-314-14	Sequence 14, Appl1
8	376	29.1	257	4	US-09-134-001C-3562	Sequence 3562, Ap
9	358.5	27.8	261	4	US-09-468-738A-29	Sequence 29, Appl
10	358.5	27.8	261	4	US-09-940-019-29	Sequence 29, Appl
11	348.5	27.0	263	4	US-09-134-001C-4512	Sequence 4512, Ap
12	341	26.4	274	4	US-09-134-001C-4431	Sequence 4431, Ap
13	330.5	25.6	258	4	US-09-504-358-12	Sequence 12, Appl
14	330.5	25.6	258	4	US-09-954-314-12	Sequence 12, Appl
15	325	25.2	333	1	US-08-440-856A-4	Sequence 4, Appl1
16	324	25.1	337	1	US-08-440-856A-3	Sequence 3, Appl1
17	319.5	24.8	256	1	US-08-594-808B-7	Sequence 7, Appl1
18	313.5	24.3	290	4	US-09-134-001C-4339	Sequence 4339, Ap
19	312.5	24.2	313	4	US-09-413-814-9	Sequence 9, Appl1
20	308.5	23.9	257	4	US-09-287-097-2	Sequence 2, Appl1
21	307.5	23.8	267	4	US-09-134-001C-5042	Sequence 5042, Ap
22	305	23.6	273	6	5512669-4	Patent No. 5512669
23	302	23.4	262	4	US-09-363-189B-6	Sequence 6, Appl1
24	294	22.8	246	3	US-09-238-481-2	Sequence 2, Appl1
25	294	22.8	246	4	US-09-572-810A-2	Sequence 2, Appl1
26	293	22.7	246	6	5229279-7	Patent No. 5229279
27	291.5	22.6	283	4	US-09-367-012-1	Sequence 1, Appl1

28	291.5	22.6	283	4	US-09-777-157A-1	Sequence 1, Appl1
29	288	22.3	243	4	US-09-239-052-2	Sequence 2, Appl1
30	288	22.3	263	4	US-09-134-001C-3505	Sequence 3505, Ap
31	281	21.8	247	1	US-08-241-766-13	Sequence 13, Appl
32	279.5	21.7	315	3	US-08-793-035-9	Sequence 9, Appl1
33	279.5	21.7	315	3	US-08-793-035-10	Sequence 10, Appl
34	273	21.2	249	4	US-08-134-001C-4825	Sequence 4825, Ap
35	271	21.1	244	1	US-08-762-129-4	Sequence 4, Appl1
36	271	21.0	263	6	5229279-4	Patent No. 5229279
37	269	20.9	244	2	US-08-762-129-3	Sequence 3, Appl1
38	268	20.8	244	2	US-09-090-567-2	Sequence 2, Appl1
39	262.5	20.3	261	4	US-08-815-225-2	Sequence 2, Appl1
40	262.5	20.3	261	4	US-08-815-225-50	Sequence 50, Appl
41	262.5	20.3	261	4	US-09-347-878-50	Sequence 50, Appl
42	260	20.2	244	1	US-08-375-962B-13	Sequence 13, Appl
43	260	20.2	244	2	US-08-562-114B-13	Sequence 13, Appl
44	260	20.2	244	4	US-08-729-594A-13	Sequence 13, Appl
45	260	20.2	244	4	US-08-937-993-13	Sequence 13, Appl

ALIGNMENTS

RESULT: 1
US-08-822-322-8
Sequence 8, Application US/08822322
Patent No. 6037158

GENERAL INFORMATION:

APPLICANT: Hummel, Werner, Riebel, Betting
TITLE OF INVENTION: Alcohol dehydrogenase and its use for
enzymatic production of chiral hydroxy compounds

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESSES:
ADDRESSEE: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York City

STATE: New York
COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

COMPUTER: IBM
OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822.322

FILING DATE: 21-March-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 196 10 984

FILING DATE: 21-March-1996

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6037158man D.

REGISTRATION NUMBER: 30,946

TELEPHONE: (212) 688-9200

TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 688-9884

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
MOLECULE TYPE: protein

US-08-822-322-8

Query Match 99.0% Score 1277, DB 3, Length 252:
Best Local Similarity 99.2% Pred. No. 5,7e-129;
Matches 250; Conservative 2; Indels 0; Gaps 0;

1 MSNRDGVKVAIIITGTTGICLAIAIKFVEKAKWITRHSQVGEKAKSVGPQIOFF 60
1 MSNRDGVKVAIIITGTTGICLAIAIKFVEKAKWITRHSQVGEKAKSVGPQIOFF 60

QY 61 QHDSDEGKTLFPATEKAFGPVSTLVNNAIGAVNKSVEETTAERKLLAVNLDGVFF 120
DB 61 QHDSDEGKTLFPATEKAFGPVSTLVNNAIGAVNKSVEETTAERKLLAVNLDGVFF 120
QY 121 GTRGIGIORMKNGKGLASIIINSSIEGFVGDPSIGAYNASKGAVRINSKSAALDCAKDXYD 180
DB 121 GTRGIGIORMKNGKGLASIIINSSIEGFVGDPSIGAYNASKGAVRINSKSAALDCAKDXYD 180
QY 181 VRVNTVHPGYIKTLPVDDLPGAEEMASORTKTPMGHIGEPNDIAYICVYLASNESKFATG 240
DB 181 VRVNTVHPGYIKTLPVDDLPGAEEMASORTKTPMGHIGEPNDIAYICVYLASNESKFATG 240
QY 241 SEFVVDGCGYTAQ 252
DB 241 SEFVVDGCGYTAQ 252

RESULT 2
US-09-466-109-8
Sequence 8, Application US/09466109
Patent No. 6225099
GENERAL INFORMATION:
APPLICANT: Hummel, Werner, Riebel, Bettina
TITLE OF INVENTION: Alcohol dehydrogenase and its use for enzymatic production of chiral hydroxy compounds
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/466,109
FILING DATE: 17-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/822,322
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6225099man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1076
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-466-109-8

Query Match 99.0%; Score 1277; DB 4; Length 252;
Best Local Similarity 99.2%; Pred. No. 5,7e-129;
Matches 250; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSNRDGVVAITIGTGLGIAIAIKFVEEGAKVMITDRHSDVGAKAKSVGTPDQIOFF 60
DB 1 MSNRDGVVAITIGTGLGIAIAIKFVEEGAKVMITDRHSDVGAKAKSVGTPDQIOFF 60
QY 61 QHDSDEGKTLFPATEKAFGPVSTLVNNAIGAVNKSVEETTAERKLLAVNLDGVFF 120
DB 61 QHDSDEGKTLFPATEKAFGPVSTLVNNAIGAVNKSVEETTAERKLLAVNLDGVFF 120

QY 121 GTRGIGIORMKNGKGLASIIINSSIEGFVGDPSIGAYNASKGAVRINSKSAALDCAKDXYD 180
DB 121 GTRGIGIORMKNGKGLASIIINSSIEGFVGDPSIGAYNASKGAVRINSKSAALDCAKDXYD 180
QY 181 VRVNTVHPGYIKTLPVDDLPGAEEMASORTKTPMGHIGEPNDIAYICVYLASNESKFATG 240
DB 181 VRVNTVHPGYIKTLPVDDLPGAEEMASORTKTPMGHIGEPNDIAYICVYLASNESKFATG 240
QY 241 SEFVVDGCGYTAQ 252
DB 241 SEFVVDGCGYTAQ 252

RESULT 3
US-08-822-322-9
Sequence 9, Application US/08822322
Patent No. 6037158
GENERAL INFORMATION:
APPLICANT: Hummel, Werner, Riebel, Bettina
TITLE OF INVENTION: Alcohol dehydrogenase and its use for enzymatic production of chiral hydroxy compounds
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,322
FILING DATE: 21-March-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 196 10 984
FILING DATE: 21-March-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6037158man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1076
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-822-322-9

Query Match 79.0%; Score 1019; DB 3; Length 251;
Best Local Similarity 80.5%; Pred. No. 2,8e-101;
Matches 202; Conservative 14; Mismatches 35; Indels 0; Gaps 0;

QY 2 SNRLDGVVAITIGTGLGIAIAIKFVEEGAKVMITDRHSDVGAKAKSVGTPDQIOFFQ 61
DB 2 SNRLDGVVAITIGTGLGIAIAIKFVEEGAKVMITDRHSDVGAKAKSVGTPDQIOFFQ 61
QY 62 HDSDDEGKTLFPATEKAFGPVSTLVNNAIGAVNKSVEETTAERKLLAVNLDGVFFG 121
DB 62 HDSDDEGKTLFPATEKAFGPVSTLVNNAIGAVNKSVEETTAERKLLAVNLDGVFFG 121
QY 122 GTRGIGIORMKNGKGLASIIINSSIEGFVGDPSIGAYNASKGAVRINSKSAALDCAKDXYD 181
DB 122 GTRGIGIORMKNGKGLASIIINSSIEGFVGDPSIGAYNASKGAVRINSKSAALDCAKDXYD 181

OY 182 RYNTVHPGTYIKTPLVDDLGAEAMSORTKTPMGIHGPNDIAYICVYLASNESEFATGS 241
Db 181 RYNTVHPGTYIKTPLVDDLGAEAMSORTKTPMGIHGPNDIAYICVYLASDETFKATGA 240

OY 242 EFVVDGGYTAQ 252
Db 241 EFVVDGGYTAQ 251

RESULT 4

US-09-466-109-9
Sequence 9, Application US/09466109
Patent No. 6225099

GENERAL INFORMATION:

APPLICANT: Hummel, Werner, Riebel, Bettina
TITLE OF INVENTION: Alcohol dehydrogenase and its use for enzymatic production of chiral hydroxy compounds

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felle & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/466,109

FILING DATE: 17-Dec-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/822,322

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6225099man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: BOER 1076

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 251 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Query Match 79.0%; Score 1019; DB 4; Length 251;

Best Local Similarity 80.5%; Pred. No. 2.8e-101;

Matches 202; Conservative 14; Mismatches 35; Indels 0; Gaps 0;

OY 2 SRRLGKVAIITGTLGIGLAITKFEVBEAKVMTDRHSVSGEAKAKSVGTPPDIOGFQ 61

Db 1 TDRLGKVAIITGTLGIGLAITKFEVBEAKVMTDRHSVSGEAKAKSVGTPPDIOGFQ 60

OY 62 HDSDEGWTLPDTEKAFGPVSTLVNNAIGAVNKSVEETTTAEWRKLLAVNLGCVFEG 121

Db 61 XXXXXXXXXXXXLPDTEKAFGPVSTLVNNAIGAVNKSVEETTTAEWRKLLAVNLGCVFEG 120

OY 122 TRLGIGRKNNKGLGASITNMSIEGFVGDPSLGAVNASKAVRIMSKSALDCAIKDYD 181

Db 121 TRLGIGRKNNKGLGASITNMSIEGFVGDPSLGAVNASKAVRIMSKSALDCAIKDYD 180

OY 182 RYNTVHPGTYIKTPLVDDLGAEAMSORTKTPMGIHGPNDIAYICVYLASNESEFATGS 241

Db 181 RYNTVHPGTYIKTPLVDDLGAEAMSORTKTPMGIHGPNDIAYICVYLASDETFKATGA 240

OY 242 EFVVDGGYTAQ 252
Db 241 EFVVDGGYTAQ 251

RESULT 5

US-08-815-225-4
Sequence 4, Application US/08815225
Patent No. 6268479

GENERAL INFORMATION:

APPLICANT: Stern, David M.

APPLICANT: Yan, Shi Du

TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE

TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING

TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/815,225

FILING DATE: 12-MAR-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/55209

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 255 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

Query Match 31.6%; Score 407.5; DB 4; Length 255;

Best Local Similarity 39.0%; Pred. No. 1.2e-35;

Matches 97; Conservative 42; Mismatches 103; Indels 7; Gaps 5;

OY 3 NRLDGKVAIITGTLGIGLAITKFEVBEAKVMTDRHSVSGEAKAKSVGTPPDIOGFQ 62

Db 2 NDLGKVAIITGTLGIGLAITKFEVBEAKVMTDRHSVSGEAKAKSVGTPPDIOGFQ 59

OY 63 DSDDEGWTLPDTEKAFGPVSTLVNNAIGAVNKSVEETTTAEWRKLLAVNLGCVFEG 122

Db 60 DSDDEGWTLPDTEKAFGPVSTLVNNAIGAVNKSVEETTTAEWRKLLAVNLGCVFEG 119

OY 123 RLGIGRKNNKGLGASITNMSIEGFVGDPSLGAVNASKAVRIMSKSALDCAIKDYD 182

Db 120 RLGIGRKNNKGLGASITNMSIEGFVGDPSLGAVNASKAVRIMSKSALDCAIKDYD 176

OY 183 RYNTVHPGTYIKTPLVDDLGAEAMSORTKTPMGIHGPNDIAYICVYLASNESEFATGS 241

Db 177 RYNTVHPGTYIKTPLVDDLGAEAMSORTKTPMGIHGPNDIAYICVYLASDETFKATGA 235

OY 242 EFVVDGGYTAQ 250

Db 236 ELAVDGGWT 244

Query Match	30.7%	Score 395.5	DB 4	Length 256
Best Local Similarity	37.7%	Pred. No. 2.3e-34		
Matches 98	Conservative 43	Mismatches 104	Indels 15	Gaps 6
3 NRDLGVAITTGTCIGIGIAATFVEGGAAGVMTDRHSVDGKRAKAVGTFDQI-QFFQ 61				
				:::

QY	4	RLOQKGAIIYGGTGLIOLATATKFEVGGAKVMITDRHSIDVGEKAKSVGPPDOL--FPQ	61
QY	11	KLKGKVMVIGGATGICGKMAEMLAAGCANIVIDLDSNIGCEPATITTSIOSGKTTSLK	70
Db	62	HOSSEDEGWTKLFDANEKAFGPVSTLVNNAAGIAVNAKSVEETTTAEWRKLLAVNLNDGVFFG	121
QY	71	LDTHLDEVAQIYDVYVREXGKIDILVNNASISIODDTENISYEEMKKEINLSLNGAFSV	130
Db	122	TRIGIORMKNKGIGASTINNSSTIEGPFVGDPS--LGAVNASKGAVRIMSKSAALDCALKDY	179
QY	131	AQGVYKRMETKSGS-SWITNVSVALGLANTODOSSETSKAGATYMLTKSLAREMS--RY	187
Db	180	DVEVNTYHPGVIYITPLVDVYFGAEAEASORTK--FPMGHIGENDIAYICVYLAASNEK	236
QY	188	GIVKNMIAIPGYMNT-----IETEKILNDNTENTPTPMERVGPEPEELAGITVYLASDASS	244
Db	237	FATGSEFYVDGQGYTA	251
QY	242	FTQGSVEFNIDGQGYTA	256

RESULT 9
US-09-468-738A-29
Sequence 29, Application US/09468738A
Patent No. 6312933
GENERAL INFORMATION:
APPLICANT: Kimoto, No. 6312933hiro
APPLICANT: Yamamoto, Hiroaki

Query Match	27.8%	Score 358.5	DB 4	Length 261
Best Local Similarity	33.9%	Pred. No. 2.2e-30		
Matches 87	Conservative 45	Mismatches 104	Indels 21	Gaps 5

RESULT 12
US-09-134-001C-4431
; Sequence 4431, Application US/09134001C
; Patent No. 6380370

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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4431
LENGTH: 274
TYPE: PRF
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4431

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Query Match          26.4%; Score 341; DB 4; Length 274;
Best Local Similarity 34.2%; Pred. No. 1.8e-28;
Matches 88; Conservative 49; Mismatches 106; Indels 14; Gaps 7;

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DB 4 RLDCRVAITIGTIGLIGLAIATKFEKCAKVMITDRHSDVGEKAKSVG-TPDOIQFQH 62
DB 5 RLEKRIAVITGASGIGASAVALAEBAHVLAD-ISDLEETVOSTINDGCKATYRV 63
DB 63 DSSDEGCTKLFDATKAFGVPSTLVNAGIAVKS-VEETTAEMRLLAVNLGDFEG 121
DB 64 DISDOKOVKPSKIEADFECHVDYFNAGVNGACRIHEPVEFEDIMAVDMGTFLV 123
DB 122 TRLGIOIRKNNGLGASTIIMSSIEGFVDPDLGAVNAKGAIRIKSAALDCAIKDQV 181
DB 124 TKLLPLPMKO--GGSIIITNASEGQADLYRSGYNAGKGVINPTKSIATIEYGRE--NI 179
DB 182 RVNTHBQYIKTPVLDLPGA--EEA-----MSORTKTPMCHIGEPNDIAYICVLAASNE 234
DB 180 RANAIAIGTIEPLVDNLAGSDEAGOTFRENCKWTPRLGRLPDEVGLVAFLASOD 239
DB 235 SKRATGSEFVVDGYTA 251
DB 240 SSFTTGTETIRIDGVMA 256

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RESULT 13
US-09-504-358-12
Sequence 12, Application US/09504358
Patent No. 6365376
GENERAL INFORMATION:
APPLICANT: Rouviere, Pierre E.
APPLICANT: Brzostowicz, Patricia C.
TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATE
FILE REFERENCE: BC1001 US NA
CURRENT APPLICATION NUMBER: US/09/504,358
CURRENT FILING DATE: 2000-02-15
EARLIER APPLICATION NUMBER: 60/120,702
EARLIER FILING DATE: 1999-February-19
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Microsoft Office 97
SEQ ID NO 12
LENGTH: 258
TYPE: PRF
ORGANISM: Brevibacterium sp HCU
US-09-504-358-12

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Query Match          25.6%; Score 330.5; DB 4; Length 258;
Best Local Similarity 33.7%; Pred. No. 2.2e-27;
Matches 91; Conservative 49; Mismatches 97; Indels 33; Gaps 8;

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DB 1 MSNRLDGKVAIITGTLGIGLAIATKFEKCAKVMITDRHSDVGEKAKSV--CTPOIQ 58
DB 4 VYDSLGADVFLVYGAGGIGKATTTALAEGRVVLTDVEDAGSQAADVRRNTNGEIR 63
DB 59 FQHDSS-----DEGWTKLFDATKAFGVPSTLVNAGIAVKSVEETTTAE 106

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DB 64 FEPLDVTNPAAVTECAKLDDEGM-----PYGLMANAGIAPSSAVDYSDEL 111
DB 107 WRKLLAVNLGVEFEFTRIGIOIRKNNGLGASIIIMSSIEGF--VGDPSLGAYNASKAVR 164
DB 112 WLRTVDINLNGVFWCCREKGRMIARGR--SVYTTSSIAGRTYSPERNAIYGATKAAYA 170
DB 165 IMKSAALDCAIKDQVRYNTHBQYIKTPVLDLPGA-AEAMSORT-KTPMGHIEPND 222
DB 171 HLVLGLGVEMA--KTGVANAVAPGYTRPTLEALKAESPEITSEWTERIPNRLNDPSE 228
DB 223 IAYICVYLAASNEKFAFGSEFVVDGYTAQ 252
DB 229 IADGVVFLMSNARIGITGVVLHIDGYTAAR 258

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RESULT 14
US-09-954-314-12
Sequence 12, Application US/09954314
Patent No. 6465224
GENERAL INFORMATION:
APPLICANT: Rouviere, Pierre E.
APPLICANT: Brzostowicz, Patricia C.
TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIA
FILE REFERENCE: BC1001 US NA
CURRENT APPLICATION NUMBER: US/09/954,314
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/120,702
PRIOR FILING DATE: 1999-February-19
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Microsoft Office 97
SEQ ID NO 12
LENGTH: 258
TYPE: PRF
ORGANISM: Brevibacterium sp HCU
US-09-954-314-12

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```

Query Match          25.6%; Score 330.5; DB 4; Length 258;
Best Local Similarity 33.7%; Pred. No. 2.2e-27;
Matches 91; Conservative 49; Mismatches 97; Indels 33; Gaps 8;

```

```

DB 1 MSNRLDGKVAIITGTLGIGLAIATKFEKCAKVMITDRHSDVGEKAKSV--CTPOIQ 58
DB 4 VYDSLGADVFLVYGAGGIGKATTTALAEGRVVLTDVEDAGSQAADVRRNTNGEIR 63
DB 59 FQHDSS-----DEGWTKLFDATKAFGVPSTLVNAGIAVKSVEETTTAE 106
DB 64 FEPLDVTNPAAVTECAKLDDEGM-----PYGLMANAGIAPSSAVDYSDEL 111
DB 107 WRKLLAVNLGVEFEFTRIGIOIRKNNGLGASIIIMSSIEGF--VGDPSLGAYNASKAVR 164
DB 112 WLRTVDINLNGVFWCCREKGRMIARGR--SVYTTSSIAGRTYSPERNAIYGATKAAYA 170
DB 165 IMKSAALDCAIKDQVRYNTHBQYIKTPVLDLPGA-AEAMSORT-KTPMGHIEPND 222
DB 171 HLVLGLGVEMA--KTGVANAVAPGYTRPTLEALKAESPEITSEWTERIPNRLNDPSE 228
DB 223 IAYICVYLAASNEKFAFGSEFVVDGYTAQ 252
DB 229 IADGVVFLMSNARIGITGVVLHIDGYTAAR 258

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RESULT 15
US-08-440-856A-4
Sequence 4, Application US/08440856A
Patent No. 5750873
GENERAL INFORMATION:
APPLICANT: DELLAORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
FILE REFERENCE: BC1001 US NA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FOERSTER

```


STREET: 2000 PENNSYLVANIA AVE. N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,856A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 05463-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1517
TELEFAX: (202) 887-0763
TELEX: 706141
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-440-856A-4

Query Match 25.28; Score 325; DB 1; Length 333;
Best Local Similarity 32.58; Pred. NO. 1.3e-26;

Matches 92; Conservative 46; Mismatches 107; Indels 38; Gaps 7;

QY 1 MSNRIDGVAITGGTIGLAIATKFEVGEAKVMTDRHSDVGEKAASVGTPOIOFF 60
DB 48 MPKRLGKVAIVTGAGIGEAIVRLFKHGAQVINDIDDAAGEALAAIG--PHYGFV 105
QY 61 QHDSDEDEGWTLEFATEKAFGPVSTLVNNAI-----AVKSVETTTAEMRKLAVNL 115
DB 106 RCDVSEEDVERAVERAVARVARGRLDVCNNAGVLCGROTRAKSILSPDAGEFDRVLRVNA 165
QY 116 DGVFEGTRIGIORMKNGKGIINNSIEGFVGPDPGLGAYNASKGAVRIMSKSALDCA 175
DB 166 LGAALGMHAAALAMTORRAG-STIISVAVAGVLGGLCPHATASKHALVGLTKNNA--CE 222
QY 176 LKDYDVRVNTVHPGYIKTPLV-----DD-----LPGAEAA---MS 207
DB 223 LGAHGIRVNCISPFVATPMLINAMRQHDASTADODADIDIDIAVPSDDEVKMEEV 282
QY 208 QRTKTPMHIGEPNPIAYICVILASNESKFAATGSEFVYDGYT 250
DB 283 RGLATLKGAITLRDIAEAALFLASDSDRYISGHNLVVDGVT 325

Search completed: April 22, 2003, 17:17:18
Job time : 20 secs

OY 241 SEFVVDGYYTAQ 252
 DB 241 SEFVVDGYYTAQ 252

RESULT 2

US-09-978-758-2
 ; Sequence 2, Application US/09978758
 ; Publication No. US20020192783A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kudooh, Masatake
 ; APPLICANT: Yamamoto, Hiroaki
 ; TITLE OF INVENTION: (R)-2-OCTANOL DEHYDROGENASES, METHODS
 ; TITLE OF INVENTION: FOR PRODUCING THE ENZYMES, AND
 ; TITLE OF INVENTION: METHODS FOR PRODUCING ALCOHOLS USING THE ENZYMES
 ; FILE REFERENCE: 06501-090001
 ; CURRENT APPLICATION NUMBER: US/09/978,758
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: PCT/JP01/01082
 ; PRIOR FILING DATE: 2001-02-15
 ; PRIOR APPLICATION NUMBER: JP 2000-374593
 ; PRIOR FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: JP 2000-43506
 ; PRIOR FILING DATE: 2000-02-16
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 254
 ; TYPE: PRT
 ; ORGANISM: Pichia finlandica
 US-09-978-758-2

Query Match 34.9%; Score 450; DB 9; Length 254;
 Best Local Similarity 39.0%; Pred. No. 1,1e-34;
 Matches 101; Conservative 46; Mismatches 100; Indels 12; Gaps 5;

OY 1 MSNRDGVAAITGGTIGLAIATKFEVEEGAKVMTD-----RHSVGEKRAKSVGTP 54
 DB 1 MSYNHNKVVAVVTGALSGISLVAKKFLQLGAKYISDVSGEKKHETVVALKAQNLMT- 59
 OY 55 DOIQFOHDSDEDEGWTKLPDATERKAGPVSITLVNAGIAVNSKEVETTTAEMKRLAVN 114
 DB 60 DNLHYVQADSKREEDNKLLISSETLATFEGDLIVCANAGICGFAPTHETPFDVKKVIAVN 119
 OY 115 LDGVFFETRLGIQRKKNKGLASITINSSIEGFGVDPDLGAVNASKGAVRIMSKSALDC 174
 DB 120 LNVFLLDKLAINWLEKSKPGVILVNMGSVHSFAAPCLAHYGAAGKGVKLLITOTLALEY 179
 OY 175 ALKQDVAVNVHGYITPLVDLPGAEEMASQRTKT-PMCHIGEPPNDIATCYVILASN 233
 DB 180 A-SHGILVNVNPGYISTPLIDEVP--KERLDKLVSLHPIGRLGRPEVADAVAFLOSO 235
 OY 234 ESKFATGESEFVVDGYYTAQ 252
 DB 236 EATFINGVSLFVVDGYYTAQ 254

RESULT 3

US-09-931-186-15
 ; Sequence 15, Application US/09931186
 ; Patent No. US20020132319A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ABBRO, MELVYN A.
 ; APPLICANT: AGREE, CHARLES S.
 ; APPLICANT: AUST, ROBERT
 ; APPLICANT: KRISINGER, CHARLES R.
 ; APPLICANT: MARGOSIAK, STEVE
 ; APPLICANT: MENG, JERRY J.
 ; APPLICANT: PELLETIER, LAURA A.
 ; APPLICANT: REJTO, PAUL A.
 ; APPLICANT: SHOMALTER, RICHARD E.
 ; APPLICANT: TEMPCZYK-RUSSELL, ANNA
 ; APPLICANT: THOMSON, JIM

APPLICANT: VANDERPOOL, DARIN
 APPLICANT: VILLAFRANCA, J. ERNEST
 TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HAD2, ITS X-RAY CRYSTAL
 TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
 TITLE OF INVENTION: OF INHIBITORS THEREOF
 FILE REFERENCE: 0125-0049
 CURRENT APPLICATION NUMBER: US/09/931,186
 CURRENT FILING DATE: 2001-08-17
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 15
 LENGTH: 253
 TYPE: PRT
 ORGANISM: Steptomyces hydrogenans
 US-09-931-186-15

Query Match 32.5%; Score 419; DB 10; Length 253;
 Best Local Similarity 39.1%; Pred. No. 9,1e-32;
 Matches 97; Conservative 42; Mismatches 103; Indels 6; Gaps 4;

OY 3 NRIDGVAAITGGTIGLAIATKFEVEEGAKVMTDRHSVGEKRAKSVGTPDOIQFOH 62
 DB 1 NDLGKTVIITGGARGLGAARQAVAGARVLAVDLEGAATARELG--DAATQHL 58
 OY 63 DSDDEGWTKLPDATERKAGPVSITLVNAGIAVNSKEVETTTAEMKRLAVNLDGVFFGT 122
 DB 59 DVTIEDMORVAVAREEGSVDLGNAGISTGMPLETESVERFRKVEINLTGVFICM 118
 OY 123 RLGIQRKKNKGLASITINSSIEGFGVDPDLGAVNASKGAVRIMSKSALDCALKQYDR 182
 DB 119 KTVIPAMKAG--GGSIVNLSAAGLGLATLSTYSGSKGKGLSLAIVE--LGTDRIR 175
 OY 183 VNTVHPGYITPLVDLPGAEEMASQRTKT-PMCHIGEPPNDIATCYVILASNESKFGTSE 242
 DB 176 VNSVHPGMYTFETMAE-TGIROEGNYPTMPGRVCEPELIGAVYKLLSDISYTTGAE 234
 OY 243 FVVDGYYT 250
 DB 235 LAVDGGWT 242

RESULT 4

US-09-954-314-14
 ; Sequence 14, Application US/09954314
 ; Patent No. US20020127866A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brozowski, Patricia C.
 ; APPLICANT: Rouviere, Pierre E.
 ; TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIA
 ; FILE REFERENCE: BC1001 US NA
 ; CURRENT APPLICATION NUMBER: US/09/954,314
 ; CURRENT FILING DATE: 2001-09-17
 ; PRIOR APPLICATION NUMBER: 60/120,702
 ; PRIOR FILING DATE: 1999-February-19
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 14
 ; LENGTH: 256
 ; TYPE: PRT
 ; ORGANISM: Brevibacterium sp HCU
 US-09-954-314-14

Query Match 30.7%; Score 395.5; DB 10; Length 256;
 Best Local Similarity 37.7%; Pred. No. 1,5e-29;
 Matches 98; Conservative 43; Mismatches 104; Indels 15; Gaps 6;

OY 3 NRIDGVAAITGGTIGLAIATKFEVEEGAKVMTDRHSVGEKRAKSVGTPDOI-OFQF 61
 DB 2 NRIDGVAAITGGAGAGMGRIOSELVASEGAVAVVADVEOEORATADAIRASGVANYWK 61
 OY 62 HDSDEGWTKLPDATERKAGPVSITLVNAGI-AVNSKEVETTTAEMKRLAVNLDGVFF 120
 DB 62 LDVDESEVELVSDIAKRFCAINVAVNAGYTGADKFTHEIDERDLDVLVSVDKGVFF 121

OY 121 CTRLCIORMKNKGASIIINMSIEGFVCPDPSICAYNASKGAVRIMSKAALDCALDKDYD 180
Db 122 MTKHCIPYFKAG-GGAYVFASTIYGLVSGOELTPYNAKGAVALFTQDAV--TYGSPN 178
OY 181 VAVNTVHPGTYKTPLY-----DLPAGEAMSORTKTPMGHIGEPNDIAYICVYLAS 232
Db 179 IAVNAVAPGTILTPVLKELGSRGPDGIDGTYTKLMG--AKHFLRGVGTPEEVAATLFLAS 236
OY 233 NESKATGSEFVVDGCTA 252
Db 237 EASFTGAVLPDGGCTA 256

RESULT 5

US-09-815-242-12688
Sequence 12688, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011a
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12688
LENGTH: 272
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12688

Query Match 28.6%; Score 369; DB 10; Length 272;
Best Local Similarity 35.8%; Pred. No. 5,1e-27;
Matches 92; Conservative 42; Mismatches 109; Indels 14; Gaps 6;

OY 4 RUDGVAITGGTGLGIALATKFEVEGAKVMTDRHSDVEKAKASVGTPOIQFQHD 63
Db 3 RLENKVAAYVTGASTGIGASAIALAGCAVYLVADIAEAVSETYDKIKNSGDKAKAYVD 62
OY 64 SDEDCWTLFLDTEKAFGVSTLVNNA--AVNKSVEETTAEMRKLAVNLGCVFPG 121
Db 63 IASGOIDNFASIRFOFGVADVLFNNAGVDMAGR--IHEPTVDYDKIMVDMRGTFLM 121
OY 122 TRLCIORMKNKGASIIINMSIEGFVCPDPSICAYNASKGAVRIMSKAALDCALDKDYD 181
Db 122 TMMLPLMNTK--GGSIVNTSSFSQADLYRSGYMAKGAVINFTKSAIEYGRD-GI 177
OY 182 RVNTVHPGTYKTPLYVDLPGAE-----AMSGRTKTPMGHIGEPNDIAYICVYLASNE 234
Db 178 RANAIAPGTIEFTPLVLDKLTGTSEDKKAPRENQKMMPTLCRLGKPEVGKLVFLASDE 237

OY 235 SKFATGSEFVVDGCTA 251
Db 238 SSFTGTIRIDGCVMA 254

RESULT 6

US-09-971-536-74
Sequence 74, Application US/09971536
Patent No. US20020159976A1
GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Havukala, Ilkka
APPLICANT: Bloksberg, Leonard
APPLICANT: Lubbers, Mark
APPLICANT: Dekker, James
APPLICANT: Christenson, Anna
APPLICANT: Holland, Ross
APPLICANT: O'Toole, Paul
APPLICANT: Reid, Julian
TITLE OF INVENTION: Lactobacillus rhamnosus Polynucleotides, Polypeptides and Me
FILE REFERENCE: 1043c2
CURRENT APPLICATION NUMBER: US/09/971,536
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/634,238
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/724,623
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: PCT/NZ01/00160
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 74
LENGTH: 261
TYPE: PRT
ORGANISM: Lactobacillus rhamnosus
US-09-971-536-74

Query Match 28.4%; Score 366.5; DB 9; Length 261;
Best Local Similarity 33.5%; Pred. No. 8.2e-27;
Matches 85; Conservative 50; Mismatches 112; Indels 7; Gaps 4;

OY 1 MSNRLDKVAITGGTGLGIALATKFEVEGAKVMT--DRHSDVEKAKASVGTPOIQ 58
Db 1 MYRDLNKGVAAYVTGSGKIGAGIAERFGEHMAVINYLGDEGAKKATDVIKNGQAV 60
OY 59 FFOHDSDEDCWTLFLDTEKAFGVSTLVNNA--AVNKSVEETTAEMRKLAVNLGCV 118
Db 61 SIHADVSTEGIASLVKTAESEFGRLDVVNNAGMEIKAPTHEVSLDDNNKYIAINQTV 120
OY 119 FFCRLCIORMKNKGASIIINMSIEGFVCPDPSICAYNASKGAVRIMSKAALDCALDK 178
Db 121 FLGRALALNTFLDHIHOPNINIISVHQIPPTFASVYAAAGSVLFTPTIMEVA--N 178
OY 179 YDVAVNTVHPGTYKTPLYVDLPGAEAMSOR--KTPMGHIGEPNDIAYICVYLASNE 236
Db 179 RGRVNAIIGPAITFP--INAEKADKAOYDQVAMIPGRLKPEVDVAGAAVLASTESS 237
OY 237 FATGSEFVVDGCT 250
Db 238 YVTGTFLEIDGCT 251

RESULT 7

US-09-815-242-5689
Sequence 5689, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.

```

US-09-815-242-11860
RESULT 9
Sequence 11860, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlssen, Karl L.
APPLICANT: Zyckind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trivick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential
FILE REFERENCE: ELTRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/206,848
PRIORITY FILING DATE: 2000-05-23
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0.0
SEQ ID NO 11860
LENGTH: 286
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa

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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22

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PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

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Query Match      26.4%; Score 340; DB 9; Length 270;
Best Local Similarity 37.1%; Pred. No. 2.7e-24;
Matches 95; Conservative 44; Mismatches 93; Indels 24; Gaps 10;

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4 RUDCKVAIIITGTLGIALIAIKFVEEGAKWITDRHSOVGEKAASVGTPOIOIOPFOHD 63

DB 6 RYAGKVVVYTGCGRGIGAGIVRAFNVCARVVICDKDESGRALEQEL--PGAN-FILCD 62
QY 64 SDEDCMFKLPDATEKAFGVSTLVNAG-IAVNVSVETTTAEMRKLAVNLDGVEFGT 122
DB 63 VFOEDVKTLYSETRIRFGHDCVNNAGHPPQRPDEETSAQGFROLLEINTLGTYLT 122
QY 123 RLGIOM-KKKIGASITNMSIEGFVGDPSLGAVNMSKAVRIMSSAALDCLKROYD 181
DB 123 KLLAPYLRISQ--NVTINISLVGAIGQAVPYVATKCAVTMTALALD--ESPFGV 177
QY 182 RVNTHPGYIKTPLVDDL-----PGA--EAMSOQTKTPMGHIGEPNDIAYICVYLAS 232
DB 178 RVNCISPGNITWTFMLMEBLALMDPRATIREGMLAQ-----PLGIMGQPAEYGAANVILAS 233
QY 233 NESKFAFGSEFVYDGC 248
DB 234 -EAMFCTGIELLVTCG 248

RESULT 12

US-09-978-697-468
Sequence 468, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kiljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James:
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
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 QY 4 RLDDKVAIIITGTLGIGIAITKEEGAKWITRHSDDVEKKAASVTPDQIQIFQND 63
 DB 6 RYAKGVVVVGTGGGIGIGIYRATVNSGARVVICDKDESGRALEQEL--PGAV-FILCD 62
 QY 64 SSDEGWTFLFDATKAFGPVSTLVNNG-IAVKSVEETTAEMRKLAVNLDDVFEGT 122
 DB 63 VTQEDDVKTLVSETIRRRGRDCVNNAGHPPQRPPEETSAGQFROLLELNLGTYTLT 122
 QY 123 RLGIQRM-KNKGIGASIIINSSIGFVGDPSLGAVNASKGAVRIMSALDCAIKDYD 181
 DB 123 KLALPYLRKSOG--NVINISLVGAIGQAQAVPVATKAVTMTKALALD--ESPGV 177
 QY 182 RVNTVHPGYIKTPLYDDJ-----PGA---EAMSQRTKTPMGHIGEPNDIAICVLYAS 232
 DB 178 RVNCISPGNIWTFPLMEELALMPDPRAPIREGMLAQ-----FLGRKGPAEYGAANVPLAS 233
 QY 233 NESKRTGSEFVYDGG 248
 DB 234 -EANFCTGIELVYTG 248
 RESULT 13
 US-09-978-192A-468
 Sequence 468, Application US/09978192A
 Patent No. US2002017753A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
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 APPLICANT: Tumas, Dandel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630PIC9
 CURRENT APPLICATION NUMBER: US/09/978, 192A
 CURRENT FILING DATE: 2001-10-15
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PRIOR FILING DATE: 1998-05-15
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Query Match      26.4%  Score 340:  DB 9:  Length 270:
Best Local Similarity 37.1%  Pred. No. 2,7e-24:
Matches 95:  Conservative 44:  Mismatches 93:  Indels 24:  Gaps 10:

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DB  6  RTAGKVVVVGGRGIGAGIVAFVNSGARVVICDKDESGRALQEL--PGAV-FILCD 62
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QY  64  SSEDGWTILFDATEKAFGPFSTLVNAG-IAVNSVEFTTAEMKLLAVNLDGVEFGT 122
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DB  63  VAGEDVAVKLVSETRIRFRRLDCVANNACHPPORPEETSAGCFQLELNLGLTYTLT 122
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QY  123  RLGIDRM-KNKGLASIIIMSSIEGFVDPDLGAYNASKAVRINSKALDCLAKDYDV 181
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DB  123  KIALPLRLKRSQ--NVINISSLVGAIGQAQAVPVATKGVATMTKALALD--ESPICV 177
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RESULT 14
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: Sequence 468, Application US/09999832A
: Publication No. US20020192706A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
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: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
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: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James;
: APPLICANT: Paonli, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
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: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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 PRIOR APPLICATION NUMBER: 60/085323
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085582
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085700
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085689
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 26.4% Score 340; DB 9; Length 270;
 Best Local Similarity 37.1% Pred. No 2,7e-24;
 Matches 95; Conservative 44; Mismatches 93; Indels 24; Gaps 10;

OY 4 RLDCVAILTGGTGLGIAIAATKFEVGEAKVYITDRHSDEKAKSVGPDOJOFPOHD 63
 DB 6 RYAGKVVVYVGGGGRGAGIARFVNSGARVICDKDESGGRLAEOL--PGAV-FILCD 62
 OY 64 SSDEGWTKLEDAFEKAFGPSTLYNNAG-IAVKSVEETTATMRKLLAVNDGVFFGT 122
 DB 63 VTQDDVKTIVSETIRREFRGLDCVYNNAGHPPQREETSAGCFRLELNLGTYYTLT 122
 OY 123 RLGIORM-KNKGIASTIINNSSIEGFVDPISLGAIVNNSKGAIVRIMSKSAALDCAKPDV 181
 DB 123 KLALPYLRKSGG---NINISSLVGAIGQAAVYVAFKGVATMTALALD--ESPRGV 177
 OY 182 RVNTHPGYIKTPLVDDL-----PGA---EANSQRTKPMGHIGEPNDIAYICVYLAS 232
 DB 178 RVNCISPGNITWPLMEIALMPDPRAVITREGMILAO-----PLGRMGCPAEVGAALAVFLAS 233
 OY 233 NESKATSEFVVDG 248
 DB 234 -EANFTGIELVYVG 248

RESULT 15
 US-09-978-189-468
 Sequence 468, Application US/09978189
 Publication No. US2003004102A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Baton, Dan
 APPLICANT: Fretara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James;
 APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
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PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
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PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
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PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
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PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
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PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-04-29
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PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640

DB 120 MSKHALKMLAAKRG-NIIMTCVSGVLVAMPDIPATYNAKSGVQLTKRMAVDYA--KHQ 176
 QY 181 VRVNTVHPGYIKTPPL-----VDLLPGA-ESAMSORIK-TPMGHIGEPNDIAYICVYLAASN 233
 DB 177 IRRVNCVCGIIDPIPLNKSEFLNNEGTLLEIKREKAKVNPLLRGRKEELIANVWLPLASD 236
 QY 234 ESKFATGSEFVVOGGYTAQ 252
 DB 237 LSSYMTGSAITADGGYTAQ 255

RESULT 5

3(or 17)beta-hydroxysteroid dehydrogenase (EC 1.1.1.51) - Comamonas testosteroni (ATCC 154129)
 C:Species: Comamonas testosteroni
 A:Variety: ATCC 11996
 C:Date: 14-Jul-1995 #sequence, revision 01-Dec-1995 #text_change 08-Oct-1999
 C:Accession: S48129; S51780; S62216; S62182
 R:Abalain, J.H.; di Stefano, S.; Amet, Y.; Quemener, E.; Abalain-Colloc, M.L.; Floch, H.
 J. Steroid Biochem. Mol. Biol. 44, 133-139, 1993
 A:Title: Cloning, DNA sequencing and expression of (3-17)beta hydroxysteroid dehydrogenase
 A:Reference number: S48129; MUID:93176721; PMID:8382516
 A:Accession: S48129
 A:Molecule type: DNA
 A:Residues: 1-254 <NBA>
 A:Cross-references: EMBL:X63379
 A:Note: The source is designated as Pseudomonas testosteroni
 R:Abalain, J.H.
 A:Reference number: S51780
 A:Accession: S51780
 A:Molecule type: DNA
 A:Residues: 1-11, 'VV', 16-254 <ABN>
 A:Cross-references: EMBL:X63379; NID:9312918; PIDN:CAA44977.1; PID:9312919
 A:Note: The source is designated as Pseudomonas testosteroni
 R:Yin, S.J.; Vagelopoulos, N.; Lundquist, G.; Joernvall, H.
 Eur. J. Biochem. 197, 359-365, 1991
 A:Title: Pseudomonas 3-beta-hydroxysteroid dehydrogenase. Primary structure and relation
 A:Reference number: S15390; MUID:91224127; PMID:2026158
 A:Accession: S15390
 A:Molecule type: protein
 A:Residues: 2-40, 'E', 41-176, 178-240, 'G', 242-254 <YIN>
 A:Note: The source is designated as Pseudomonas testosteroni
 R:Bench, J.; Knapp, S.; Oppermann, U.C.T.; Haegglund, O.; Joernvall, H.; Ladenstein, R.
 Eur. J. Biochem. 236, 144-148, 1996
 A:Title: Crystallization and crystal packing of recombinant 3 (or 17) beta-hydroxysteroid
 A:Reference number: S62216; MUID:96184891; PMID:8617258
 A:Accession: S62216
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 2-254 <BEN>
 R:Bocco, J.L.; Panzetta, G.; Actis, L.A.; Gentl-Raimondi, S.
 submitted to the EMBL Data Library, July 1993
 A:Description: Nucleotide sequence of the beta-hydroxysteroid dehydrogenase from Pseudom
 A:Reference number: S62182
 A:Accession: S62182
 A:Molecule type: DNA
 A:Residues: 1-40, 'E', 41-176, 178-254 <BOC>
 A:Cross-references: EMBL:L08971; NID:9309859; PIDN:AA25742.1; PID:9309860
 A:Note: The source is designated as Pseudomonas testosteroni
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 C:Keywords: oxidoreductase
 F:8-185/Domain: 3(or 17)beta-hydroxysteroid dehydrogenase #status experimental <MNT>
 F:8-185/Domain: short-chain alcohol dehydrogenase homology <SABH>

Query Match

Best Local Similarity 30.5%; Score 393; DB 2; Length 254;
 Matches 92; Conservative 49; Mismatches 100; Indels 10; Gaps 6;

QY 1 MSNRDQKVAITGCTGLAIGLAITAFVEEGARVMTDRHSVDGKRAKSVGTPDOIFP 60
 DB 1 MTRNLOGKVALVYGASVGLLEVKKLLTGAGAVAFSDINA-AGQOLAELG--ERSMFV 57

QY 61 QHSDSDGCKTLFDATEKAGPSTLVNNAIGAVNKSVEETTTAEVRKLLAVNLDCVFF 120
 DB 58 RHVSSPADMTLVMAAORRLGTLNVLNNAIGILLPGDMETGRLEDSRLKINTSEVFI 117
 QY 121 CTRGLGTRMKRKGKASIIINSSITEGVDPISLCAVYNAKSAALDCAKDLYD 180
 DB 118 GCOOGIAAME--TGGSIINAVASVMLPIEOYAGYSKSAVSAITRAALSCRKGYA 175
 QY 181 V-RVNTVHPGYIKTPPLVD-DLP--GAEAMSORIK-TPMGHIGEPNDIAYICVYLAASN 235
 DB 176 IRRVNCVCGIIDPIPLNKSEFLNNEGTLLEIKREKAKVNPLLRGRKEELIANVWLPLASD 236
 QY 236 KFAFGSEFVVD 246
 DB 236 SVMSGSELHAD 246

RESULT 6

547055
 hypothetical protein 5 - Xanthobacter sp.
 C:Species: Xanthobacter sp.
 C:Date: 19-Mar-1997 #sequence, revision 19-Mar-1997 #text_change 05-Nov-1999
 C:Accession: S47055
 R:Swaving, J.; Weijers, C.A.G.M.; van Ooyen, A.J.J.; de Bont, J.A.M.
 submitted to the EMBL Data Library, June 1994
 A:Description: Plamentation of Xanthobacter Py2 mutants in epoxylkane degradation:
 A:Reference number: S47051
 A:Accession: S47055
 A:Molecule type: DNA
 A:Residues: 1-249 <SWA>
 A:Cross-references: EMBL:X79863; NID:9520947; PIDN:CAA56245.1; PID:9520952
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 F:5-181/Domain: short-chain alcohol dehydrogenase homology <SABH>

Query Match

Best Local Similarity 30.3%; Score 391; DB 2; Length 249;
 Matches 98; Conservative 39; Mismatches 105; Indels 10; Gaps 6;

QY 5 LDGKVALITGCTGLAIGLAITAFVEEGARVMTDRHSVDGKRAKSVGTPDOIFQCHDS 64
 DB 2 LDGKVALITGCTGLAIGLAITAFVEEGARVMTDRHSVDGKRAKSVGTPDOIFQCHDS 64
 QY 65 SDEGKTKLDATEKAGPSTLVNNAIGAVNKSVEETTTAEVRKLLAVNLDCVFF 124
 DB 60 TDEAIIITAMAGAGORALGIPITMAATCAKCAVAVNLTRQMAADYSGR--GIKVN 119
 QY 125 GIORMKKKGASIIINSSITEGVDPISLCAVYNAKSAALDCAKDLYDVRVN 184
 DB 120 ALFGMLERKGA-IVNCGSVAGLGIPTMAATCAKCAVAVNLTRQMAADYSGR--GIKVN 176
 QY 185 TVHPGYIK-TPLVDDLPAGE--EAMSOR-TKTPMGHIGEPNDIAYICVYLAASNESKFAT 239
 DB 177 VVCGPSTVAGIDMGKQLGCTCDELEKRLAKTPMGFGIPEDIAEAVALILSTKAFTV 236
 QY 240 GSEFVVDGTYA 251
 DB 237 GSVLAVDGGMTA 248

RESULT 7

E72427
 oxidoreductase, short chain dehydrogenase/reductase family - Thermotoga maritima (s
 C:Species: Thermotoga maritima
 C:Date: 11-Jun-1999 #sequence, revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: E72427
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; H
 Garret, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genom
 A:Reference number: A72200; MUID:99287316; PMID:10360571
 A:Accession: E72427

C:Accession: B95284
 R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
 K.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
 Proc. Natl. Acad. Sci. U.S.A. 99, 9883-9888, 2001
 A:Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti*
 A:Reference number: A95262; MUID:21396509; PMID:11481432
 A:Accession: B95284
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-253 <KUR>
 A:Cross-references: GB:AE006469; PIDN:AK64836.1; PID:g14523249; GSPDB:GN00165
 A:Experimental source: strain 1021, megaplasmid pSYMA
 R:Galibert, F.; Flann, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebutel, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: SMO329
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 28.9%; Score 372.5; DB 2; Length 253;
 Best Local Similarity 37.7%; Pred. No. 2.4e-22;
 Matches 97; Conservative 46; Mismatches 93; Indels 21; Gaps 8;

OY 1 MSNRDGVVAITGCTGLGATATKFEVBEKAWITDRH-----SDVGEKAAKSVGTPD 56
 1 MSKRPDGVVAITGCTGLGATATKFEVBEKAWITDRH-----SDVGEKAAKSVGTPD 55
 DB 1 MSKRPDGVVAITGCTGLGATATKFEVBEKAWITDRH-----SDVGEKAAKSVGTPD 55
 OY 57 IQOFPOHSDDEGWTKLFDATKAFQPVSTLVNNAIGAVNKSVEETTTAEKRLAVLND 116
 DB 56 SGIRVANNVSRDCCALVATVERFGRIDTVNNAIGAVNKSVEETTTAEKRLAVLND 115
 OY 117 GVFEGTRIGIORMK-NKGIGASTINMSIEGFVGDPSLGAVNASKAVRINMSKAAALDCA 175
 DB 116 GVFVMSRAVAVPLKTKTKG--SIVNIGSVSSLGGMASHAVNAGGVANLTTRSA--CD 170
 OY 176 LKDYDVAVNTVHPGYIKTPLVVDLPAGEAMSGRT--KTPMGHIGEPNDIAYICVYLASN 233
 DB 171 LGRKGVANVTAPGLTGVGMVRAIMD-DDALLEKANDRIPLRRAGOP--ASAVAFILASD 226
 OY 234 ESKFATGSEFVVDGGYT 250
 DB 227 EAAMTGTITLFDAGCMT 243

RESULT 11
 JS0385
 glucose 1-dehydrogenase (EC 1.1.1.47) - *Bacillus megaterium*
 C:Species: *Bacillus megaterium*
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jun-1999
 R:Accession: J39852; JS0385
 R:Matsuura, T.; Ebara, R.V.; Nakai, T.; Makino, Y.; Negoro, S.; Urabe, I.; Okada, H.
 J. Ferment. Bioeng. 70, 363-369, 1990
 A:Title: Structure of isozyme genes of glucose dehydrogenase from *Bacillus megaterium* IA
 A:Reference number: J39850
 A:Accession: J39852
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-261 <RES>
 A:Cross-references: GB:D90043; NID:g216265; PIDN:BA014099.1; PID:g216268
 A:Experimental source: strain IAM1030
 C:Complex: homotetramer
 C:Function:
 A:Description: catalyzes NAD(P)-dependent dehydrogenation of D-glucose.
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 C:Keywords: oxidoreductase
 F:8-189/Domain: short-chain alcohol dehydrogenase homology <SAND>

Query Match 28.8%; Score 371.5; DB 2; Length 261;
 Best Local Similarity 34.2%; Pred. No. 3e-22;
 Matches 88; Conservative 51; Mismatches 105; Indels 13; Gaps 5;

OY 1 MSNRDGVVAITGCTGLGATATKFEVBEKAWITDRHSDVGEK-----ASVGP 54
 1 MSKRPDGVVAITGCTGLGATATKFEVBEKAWITDRHSDVGEK-----ASVGP 56
 DB 1 MSKRPDGVVAITGCTGLGATATKFEVBEKAWITDRHSDVGEK-----ASVGP 56
 OY 55 DQIOFPOHSDDEGWTKLFDATKAFQPVSTLVNNAIGAVNKSVEETTTAEKRLAVLND 114
 DB 57 GEAIAKAGDVTVESDVINLVOSSTKEKGLDMINNAIGAVNKSVEETTTAEKRLAVLND 116
 OY 115 LQGFEGTRIGIORMKNGIGASTINMSIEGFVGDPSLGAVNASKAVRINMSKAAALDCA 174
 DB 117 LQGFEGTRIGIORMKNGIGASTINMSIEGFVGDPSLGAVNASKAVRINMSKAAALDCA 176
 OY 175 AKDYDVAVNTVHPGYIKTPLVVDLPAGEAMSGRT--KTPMGHIGEPNDIAYICVYLASN 233
 DB 177 AKR--GIRVANNIGPAINTPINAEKFADEQRAVDESIMPVGIPEPEIAVAAMVLASS 234
 OY 234 ESKFATGSEFVVDGGYT 250
 DB 235 EASYVTGITLFDAGCMT 251

RESULT 12
 A33528
 glucose 1-dehydrogenase (EC 1.1.1.47) - *Bacillus megaterium*
 C:Species: *Bacillus megaterium*
 C:Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 11-Jun-1999
 R:Accession: A33528
 R:Makino, Y.; Negoro, S.; Urabe, I.; Okada, H.
 J. Biol. Chem. 264, 6381-6385, 1989
 A:Title: Stability-increasing mutants of glucose dehydrogenase from *Bacillus megate*
 A:Reference number: A33528; MUID:89197943; PMID:2495285
 A:Accession: A33528
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-261 <MAK>
 A:Cross-references: GB:J04805; NID:g142974; PIDN:AAA22475.1; PID:g142975
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 C:Keywords: oxidoreductase
 F:8-189/Domain: short-chain alcohol dehydrogenase homology <SAND>

Query Match 28.7%; Score 370.5; DB 2; Length 261;
 Best Local Similarity 33.6%; Pred. No. 3.6e-22;
 Matches 86; Conservative 51; Mismatches 108; Indels 11; Gaps 4;

OY 1 MSNRDGVVAITGCTGLGATATKFEVBEKAWIT-----DRHSDVGEKAAKSVGTPD 55
 1 MSKRPDGVVAITGCTGLGATATKFEVBEKAWIT-----DRHSDVGEKAAKSVGTPD 56
 DB 1 MSKRPDGVVAITGCTGLGATATKFEVBEKAWIT-----DRHSDVGEKAAKSVGTPD 56
 OY 56 QIOFPOHSDDEGWTKLFDATKAFQPVSTLVNNAIGAVNKSVEETTTAEKRLAVLND 115
 DB 61 AV---KGVTVESDVINLVOSSTKEKGLDMINNAIGAVNKSVEETTTAEKRLAVLND 117
 OY 116 DGVFEGTRIGIORMKNGIGASTINMSIEGFVGDPSLGAVNASKAVRINMSKAAALDCA 175
 DB 118 TGAFGLSREAIKFEVENDIGVAINMSVHEKIPVLEVHAASGKMKMTETLALLEYA 177
 OY 176 LKDYDVAVNTVHPGYIKTPLVVDLPAGEAMSGRT--KTPMGHIGEPNDIAYICVYLASN 234
 DB 178 PK--GIRVANNIGPAINTPINAEKFADEQRAVDESIMPVGIPEPEIAVAAMVLASS 235
 OY 235 SKFATGSEFVVDGGYT 250
 DB 236 ASYVTGITLFDAGCMT 251

RESULT 13
 B86737
 acetoin dehydrogenase (EC 1.1.1.5) [imported] - *Lactococcus lactis* subsp. *lactis* (s

Query Match	28.54	Score 368	DB 2:	Length 253
Best Local Similarity	34.38	Pred. No. 5.4e-22		
Matches	86	Conservative	48	Mismatches 103; Indels 14; Gaps 4
QY	8	KVAIIITGCTLGIGAIATKFEVEEGAKVMYITDRHSVDGEAKAKSVGTPDQIQFOHQHSDSE	67	
		: : : :		
Db	3	KIAVATGCGGIGCAIIRKRLYNDGFKVAIIDYNEETQOKAKETGL-ENSAFALKADYSOR	60	
QY	68	DGMYTLDATEAKGAPVSTLVNNGAGIVNKSVEBETTAERKLLAVLQDVSFEFGTRLGIO	127	
Db	61	EQVISAALNAVVDKFGDGLVNVVNNAGIPIPTQIETITPEQFHQYVNIINAGVGLMTGTSTRA	120	
QY	128	RMKKKIGASITNNKSTIEGFGDPSLCAVYAAKSGAVARINSKALCALCKLDYDVRYNTVA	187	
Db	121	LFRRLGIGGKRIINATSOAGVYGNPNMLTLYSSSKFAFVGMTQIARD-LAEEGITVNAVYA	178	
QY	188	PGYIKTFLVYDL-----PGAEEAMSOR---KTPMGHGEENIDAIYICVYLASNEKF	237	
		: : : : : :		
Db	179	PGIATKTPMMDIAHQVKGKNNKGDDEMGQIFAFADIAMKRLSEFEDVNAVYSLFAGDSMT	238	
QY	238	ATGSEFVVDGG	248	
Db	239	ITGGTIIIVDGG	249	

Query Match	28.48;	Score 367;	DB 2;	Length 258;
Best Local Similarity	35.7%;	Pred. No. 6.7e-22;		
Matches	92;	Conservative 45;	Mismatches 105;	Indels 16;
				Gaps 7.

RESULT 15
A99950
hypothetical protein SA2260 [imported] - *Staphylococcus aureus* (strain N315)
C:Species: *Staphylococcus aureus*
C:Date: 10-May-2001 #sequence,revision 10-May-2001 #text,change 22-Oct-2001
C:Accession: A99950
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, ma, A.; Mitani-Tani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimura, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiwamatsu, K.
L:ncnt 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: A99950
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-272 <KUR>
A:Cross-references: GB:BA000018; PID:g13702422; PIDN:BA843563.1; GSPDB:GM00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA2260
A:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homolog

Search completed: April 22, 2003, 17:16:52
Job time : 22 secs

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 17:12:56 ; Search time 13 Seconds
(without alignments)
804.003 Million cell updates/sec

Title: US-09-910-033A-2

Sequence: 1290 1 MSNRRLDGVKVAITRGCTIG.....NESKFRATGSEFVVDGGYTAQ 252

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	464.5	36.0	260	1 YK02_MYCTU	Q10855 pseudocacteri
2	441.5	34.2	250	1 LK02_PSEPA	P50198 pseudomonas
3	407.5	31.6	255	1 2BHD_STREX	P19992 streptomyc
4	400.5	31.0	255	1 YKFD_BACSU	P39640 bacillus su
5	383	29.7	256	1 Y019_THEMA	Q56318 thermotoga
6	380	29.5	247	1 YD50_MYCTU	Q11020 mycobacteri
7	371.5	28.8	261	1 DHG1_BACME	P39482 bacillus me
8	370.5	28.7	253	1 DHG_BACME	P40288 bacillus me
9	370	28.7	253	1 3BHD_COMTE	P19871 comamonas t
10	365.5	28.3	246	1 FABG_THEMA	Q9X248 thermotoga
11	363.5	28.2	261	1 DHGA_BACME	P10528 bacillus me
12	360	27.9	262	1 DHGB_BACME	P07999 bacillus me
13	358.5	27.8	261	1 DHG_BACSU	P12310 bacillus su
14	357.5	27.7	261	1 DHG4_BACME	P39485 bacillus me
15	355.5	27.6	261	1 DHG2_BACME	P39483 bacillus me
16	352.5	27.5	261	1 DHG3_BACME	P39484 bacillus me
17	351.5	27.2	251	1 Y325_THEMA	Q9WY90 thermotoga
18	348.5	27.0	258	1 DHG2_BACSU	P80869 bacillus su
19	345	26.7	261	1 DHB8_HUMAN	Q92506 homo sapien
20	339.5	26.3	256	1 BUDC_KLEPN	Q48436 klebsiella
21	326	25.3	285	1 GS39_BACSU	P80873 bacillus su
22	325.5	25.2	260	1 DHB8_MOUSE	P50171 mus musculu
23	324	25.1	336	1 T52_MAIZE	P50160 zeamays (m
24	322	25.0	289	1 YHDF_BACSU	Q00750 bacillus su
25	321	24.9	248	1 FABG_CHLNU	Q9PK77 chlamydia s
26	321	24.9	248	1 Y4VI_RHISN	Q53217 rhizobium s
27	319.5	24.8	256	1 GNO_GLUOX	P50199 gluconobact
28	319.5	24.8	258	1 BDHA_RHIME	Q86034 vibriobium m
29	318	24.7	244	1 FABG_VIBCH	Q9KQ77 vibrio chol
30	317.5	24.6	262	1 VER1_ASPPA	P50161 aspergillus
31	317	24.6	241	1 PHBB_ZOORA	P23238 zoogloea ra
32	316	24.5	246	1 FABG_BACSU	P51831 bacillus su
33	316	24.5	281	1 SOUL_CANAL	P87219 candida alb

34	313.5	24.3	264	1 STCU_EMENT	Q00791 emeticella
35	312	24.2	241	1 PHBB_RHIME	P50205 rhizobium m
36	312	24.2	248	1 FABG_AQUAE	O67610 aquifex aeo
37	310.5	24.1	271	1 SDRI_PICAB	O08632 picea abies
38	310	24.0	273	1 TRN1_DARTS	P50162 datura stra
39	307.5	23.8	250	1 LINC_PSEPA	P50197 pseudomonas
40	305	23.6	247	1 FABG_CHLFR	P38004 chlamydia t
41	305	23.6	285	1 YHXC_BACSU	P40397 bacillus su
42	304.5	23.6	248	1 FABG_CHLNU	Q948P2 chlamydia s
43	303	23.5	278	1 Y4LA_RHISN	P55541 rhizobium s
44	301.5	23.4	320	1 FABG_CUPLA	P28643 cuphea lanc
45	299.5	23.2	253	1 Y4MP_RHISN	P55575 rhizobium s

ALIGNMENTS

RESULT 1	ID	YK02_MYCTU	STANDARD	PRT	260 AA.
AC	Q10855:				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	15-JUL-1999 (Rel. 38, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Putative oxidoreductase RV2002 (EC 1.-.-.-)				
GN	FABG3 OR RV2002 OR MT2058 OR MTCY39.16C.				
OS	Mycobacterium tuberculosis.				
OC	Bacteria: Actinobacteria: Actinobacteriia (class): Actinobacteridae;				
OX	Actinomycetales: Corynebacterineae; Mycobacteriaceae; Mycobacterium.				
NCBI_TaxID=1773;					
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-H37RV;				
RX	MEDLINE:98295987; PubMed-9634230;				
RA	Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,				
RA	Gordon S.V., Eiglmeier K., Gao S., Barry C.E. III, Telata F.,				
RA	Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,				
RA	Davies R., Devlin K., Jagsels K., Krogan A., McLean J., Moule S., Murphy L.,				
RA	Hornsby T., Jagsels K., Krogan A., McLean J., Moule S., Murphy L.,				
RA	Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,				
RA	Rutler S., Seeger K., Skelton S., Squares S., Squares R.,				
RA	Sulton J.E., Taylor K., Whitehead S., Barrell B.G.,				
RT	"Deciphering the biology of Mycobacterium tuberculosis from the				
RT	complete genome sequence."				
RT	Nature 393:537-544(1998).				
RL	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-CDC 1551 / Oshkosh;				
RA	Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,				
RA	Petersen J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,				
RA	Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,				
RA	Delcher A., Uitterback T., Weldman J., Khoult H., Gill J., Mikule A.,				
RA	Bisai W.;				
RT	"Whole genome comparison of Mycobacterium tuberculosis clinical and				
RT	laboratory strains."				
RT	Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.				
RL	-i- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES				
CC	(SDS) FAMILY.				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
CC	EMBL: 274025; CAA98414.1; -				
DR	EMBL: AE007057; AAK46335.1; -				
DR	HSSP: P19992; IHDC.				
DR	TIGR: MT2058; -				
DR	TubercuList: RV2002; -				
DR	InterPro: IPR002198; ADH_short.				

DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR Hypothetical protein: Oxidoreductase: NAD: Complete proteome.
 FT ACT_SITE 153 153 NAD (By SIMILARITY).
 FT CONFLICT 174 174 S -> G (IN REF. 2).
 FT SEQUENCE 260 AA; 27030 MW; 0935A14ED36220B7 CRC64;

Query Match 36.0%; Score 464.5; DB 1; Length 260;
 Best Local Similarity 42.2%; Pred. No. 6,6e-31;
 Matches 106; Conservative 44; Mismatches 90; Indels 11; Gaps 5;

OY 1 MSNRLDGKVAITTGTLGIGLAIAATKEVEGAKVMITDRHSVGEKAASVGPDPDIOFE 60
 DB 1 MSGRIGKVALVSGARGSGASHVAMVEGAKVFGDLDEGKVAELA--DAARV 58
 OY 61 OHSSDEDCGWTLPDTEKAFGPVSTLVNAGIAVKNKSVETTTAEWRKLLAVNLGVEF 120
 DB 59 HLDVTPQAWMTAVDPATVATFAGLHVNLNAGILMGTIEDYALTEMORILLDNLGVFL 118
 OY 121 GTRIGIQRKKNKGLASIIINMSIEGFGVDPISLGAIVNASKAVRIMSKAALDCAKD 180
 DB 119 GTRAVVKKPKKRG--SIINISIEGLACTVACHGTATKFAVRGLTKSTALE--LGPSG 175
 OY 161 VRVNTVHPGTYKTPVLDLPGAEAMSORTKTPMGHIGEPNDIAYICVYLASNEKFAFG 240
 DB 176 IRVNSIHGLVTPMTDWP--EDIF---GTALGRAAEVPSNLYVLADDESSYSIG 229
 OY 241 SEFVVDGCVTA 251
 DB 230 AEFVVDGCVTA 240

RESULT 2

LINK_PSEPA
 ID LINK_PSEPA STANDARD: PRT: 250 AA.

AC P50198;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE 2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (EC 1.1.-.-)
 GN (2,5-DOL dehydrogenase).
 LN LINK.

OS Pseudomonas paucimobilis (Sphingomonas paucimobilis).
 OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
 OC Sphingomonas.

OX NCBI_TaxID=13689;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=UT26;
 RX MEDLINE=94252977; PubMed=7515041;

RA Nagata Y., Ohtomo R., Miyachi K., Fukuda M., Yano K., Takagi M.;

RT Cloning and sequencing of a 2,5-dichloro-2,5-cyclohexadiene-1,4-diol

RT dehydrogenase gene involved in the degradation of gamma-

RT hexachlorocyclohexane in Pseudomonas paucimobilis.*;

RL J. Bacteriol. 176:3117-3125(1994).

CC -1- FUNCTION: DEGRADATION OF 2,5-DICHLORO-2,5-CYCLOHEXADIENE-1,4-DIOL

CC (2,5-DDOL) INTO 2,5-DICHLOROHYDROQUINONE (2,5-DCHQ). LINK IS NOT

CC ESSENTIAL TO GAMMA-HCH DEGRADATION.

CC -1- SIMILARITY: DEGRADATION OF GAMMA-HEXACHLOROCYCLOHEXANE.

CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES

CC (SDR) FAMILY.

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DR EMBL: D23722; BAA04939.1; -

DR HSPR: P19992; IHNC.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR Aromatic hydrocarbons catabolism; Oxidoreductase: NAD.
 FT ACT_SITE 156 156 NAD (By SIMILARITY).
 FT SEQUENCE 250 AA; 25492 MW; 8C52703FF76382CF CRC64;

Query Match 34.2%; Score 441.5; DB 1; Length 250;
 Best Local Similarity 41.0%; Pred. No. 4,7e-29;
 Matches 105; Conservative 43; Mismatches 93; Indels 15; Gaps 6;

OY 1 MSNRLDGKVAITTGTLGIGLAIAATKEVEGAKVMITDRHSVGEKAASV-----GTPD 55
 DB 1 MANRLAGKVALITGASGIGAAAKRAFAEGAKVY----GDLNEEMAKGVVAEIRIAGG 56
 OY 56 QIQFOHSSDEDCGWTLPDTEKAFGPVSTLVNAGIAVKNKSVETTTAEWRKLLAVNL 115
 DB 57 DALFTRLDVTDAASNNIAAIVDGGGLTTLNATGIIHPGFEESIEGNNKVAANQ 116
 OY 116 DGVFETRLGIQRMKNKGLASIIINMSIEGFGVDPISLGAIVNASKAVRIMSKAALDCA 175
 DB 117 TAFIFGKAIPELVKSGNG--SIINISLIGMFPAGNASYCATRAAVIMSKAALD-- 173
 OY 176 LKDYVRVNTVHPGTYKTPVLDLPGAEAMSORTKTPMGHIGEPNDIAYICVYLASNE 234
 DB 174 FVDRGVVNTVHPGGMNPTITANVP--PDVLKQRTSOLPMKLGDPIDIANCALFLASE 231
 OY 235 SKFATSEFVVDGCVTA 250
 DB 232 AKYITGVLDLPIDGWS 247

RESULT 3

2BHD_STREX
 ID 2BHD_STREX STANDARD: PRT: 255 AA.

AC P19992;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE 20-beta-hydroxysteroid dehydrogenase (EC 1.1.1.53).
 GN Streptomyces exfoliatus (Streptomyces hydropneus).
 LN Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Streptomycetaceae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=1905;
 RN [1]

RP SEQUENCE.

RC MEDLINE=90306362; PubMed=2194840;

RA Marekov L., Krook M., Joernvall H.;

RT "Prokaryotic 20 beta-hydroxysteroid dehydrogenase is an enzyme of the

RT 'short-chain, non-metalloenzyme' alcohol dehydrogenase type.*;

RL FEBS Lett. 266:51-54(1990).

RL [2]

RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).

RX MEDLINE=92052211; PubMed=1946424.

RA Ghosh D., Weeks C.M., Grochulski P., Duax W.L., Ertman M.,

RT Rimsay R.L., Orr J.C.;

RT "Three-dimensional structure of holo 3 alpha,20 beta-hydroxysteroid

RT dehydrogenase: a member of a short-chain dehydrogenase family.*;

RL Proc. Natl. Acad. Sci. U.S.A. 88:10064-10068(1991).

CC -1- CATALYTIC ACTIVITY: Androstane-3-alpha,17-beta-diol + NAD(+) - 17-

CC beta-hydroxyandrostane-3-one + NADH.

CC -1- SUBUNIT: HOMOTETRAMER.

CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES

CC (SDR) FAMILY.

DR PIR: S10707; S10707.

DR PDB: 2HSD; 3I-AUG-94.

DR PDB: 1HDC; 07-FEB-95.

DR InterPro: IPR002198; ADH_short.

DR Pfam: PF00106; adh_short; 1.

DR PRINTS: PR00080; SDRFAMILY.

DR PROSITE: P500061; ADH_SHORT; 1.
 KW Oxidoreductase: NAD: Steroid metabolism; 3D-structure.
 FT NP_BIND 10 34 NAD (BY SIMILARITY).
 FT ACT_SITE 152 152
 SO SEQUENCE 255 AA; 26484 MW; 9CB93CB66AA628D5 CRC64;
 Query Match 31.6%; Score 407.5; DB 1; Length 255;
 Best Local Similarity 39.0%; Pred. No. 2.9e-26;
 Matches 97; Conservative 42; Mismatches 103; Indels 7; Gaps 5;
 OY 3 NMLDQKVAITITGTLGIAIAATKFEVEGAKVMTDRHSVDGEKAASVGTPOIOFQ 62
 DB 2 NLSGCTVITITGARGLGAEARQAVAGARVLAADVDEGATARELG--DAARQHL 59
 OY 63 DSSDEDGNTKLPDATEKAFGPVSTLVNAGIAVANKSVEETTTAEMRKLLAVNLGVEFT 122
 DB 60 DVTEEDMORVAVAYAREEGSGVDGLVNNAGISITGMELETESVERFRKVDINTLTCVITGM 119
 OY 123 RLGIONMKKKGASTIINNSIEGFPDPSLGAVNASKGAVRIMSKAALCALKDQYVR 182
 DB 120 KTVIPPMKRG--GGSTIVNISAAGLWGLALTSSYGASKMGVRLSKLAAVE--LQTDRI 176
 OY 183 VNTVHPGYIKTFLVDLPAGEAASQRTKTPMGHIG-EPNDIAVICYVLASNESKFGATG 241
 DB 177 VASVHPGMYTMTAE--TGIRQEGVNPNTPMGRVGNBPETIAGAVYKLLSDTSYVTGA 235
 OY 242 EFVVDGGYTP 250
 DB 236 ELAVDGGMT 244
 RESULT 4
 ID YWFD_BACSU STANDARD; PRT; 255 AA.
 AC P39640;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical oxidoreductase ywfd (EC 1.-.-.-).
 GN YWFD OR IPA-82D.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
 OX NCBI_TaxId=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=95020537; PubMed=7934828;
 RA Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales M.,
 RA Hullu M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,
 RA Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,
 RA Rapoport G., Danchin A.;
 RA "Bacillus subtilis genome project: cloning and sequencing of the 97
 kb region from 325 degrees to 333 degrees.";
 RT Mol. Microbiol. 10:371-384(1993).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertoletti M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borriss R., Boursier L., Bruns A., Braun M., Bridgell S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capiano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerion I.F., Cummings S.D., Daniel R.A.,
 RA Denzot F., Devigne K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.A.,
 RA Entlan K.D., Erlington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizli A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Heaut A.,
 RA Hilbert H., Holtsappel S., Hosono S., Hullu M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koeltter P., Koningsstein G., Krogsh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Pario V., Pohl T.M., Portetelle D., Porvillat S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Roche A., Roche B., Rose M., Sadale Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Soldo B.,
 RA Sekiguchi J., Sekowska A., Seror S.D., Serro P., Shin B.S., Soldo B.,
 RA Sorokin A., Taccout E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpsita P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarelli A.,
 RA Viari A., Wambolt R., Wedler E., Wedler H., Weltzenegger T., Yata K.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 subtilis.";
 RL Nature 390:249-256(1997).
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 CC EMBL: X73124; CAA51638.1;
 CC EMBL: 299123; CAB5799.1;
 CC PIR: S39737; S39737.
 CC HSSP: P50162; IAEI.
 CC Subtilist; BG10628; ywfd.
 CC InterPro: IPR002198; ADH_short.
 CC Pfam: PF00106; adh_short; 1.
 CC PRINTS: PR00080; SDRFAMILY.
 CC PROSITE: P500061; ADH_SHORT; 1.
 CC NP_BIND 11 154
 CC Hypothetical protein; Oxidoreductase; Complete proteome.
 CC FT ACT_SITE 154 154
 CC BY SIMILARITY.
 SO SEQUENCE 255 AA; 27324 MW; 20AA2259BF88C9B CRC64;
 Query Match 31.0%; Score 400.5; DB 1; Length 255;
 Best Local Similarity 37.1%; Pred. No. 1.1e-25;
 Matches 96; Conservative 45; Mismatches 107; Indels 11; Gaps 6;
 OY 1 MSNRDQKVAITITGTLGIAIAATKFEVEGAKVMTDRHSVDGEKAASVGTPOIOF 60
 DB 1 MINNLDKTYLVITGARGLGAEARQAVAGARVLAADVDEGATARELG--DAARQHL 59
 OY 61 QHDSDEDGNTKLPDATEKAFGPVSTLVNAGIAVANKSVEETTTAEMRKLLAVNLGVEFT 120
 DB 60 QDTDEAAGQAHAVESAVHFGGLDVLNNGIETVAPIHHEWELSDMNKVLQVNLGML 119
 OY 121 GTRLGIOBMKKGASTIINNSIEGFPDPSLGAVNASKGAVRIMSKAALCALKDQYVR 180
 DB 120 MSKHALKHLMLAAGRG-NIINTCSVGLVAMPDIPAVNASKGGLVLTSMADVA--KIQ 176
 OY 181 VRVNTVHPGYIKTFLVDLPAGEAASQRTKTPMGHIGEPNDIAVICYVLASN 233
 DB 177 IIRNCVCPGLIDPPLNKSFLNNEGTLIEIKKERAKYNPLRLQKPEIARVAMPLASD 236
 OY 234 ESKFATGSEFVVDGGYTAQ 252
 DB 237 LSSYMTGSAITADGGYTAQ 255
 RESULT 5
 ID Y019_THEMEA STANDARD; PRT; 256 AA.
 AC Q56318;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Putative oxidoreductase TM0019 (EC 1.-.-.-).
GN TM0019.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogae (class); Thermotogales;
OC Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB / DSM 3109;
RX MEDLINE=96125254; PubMed=8550425;
RT Kletzin A., Adams M.;
RT Molecular and phylogenetic characterization of pyruvate and 2-
RT ketosulfolactate ferredoxin oxidoreductases from *Pyrococcus furiosus*
RT and pyruvate ferredoxin oxidoreductase from *Thermotoga maritima*.
RL J. Bacteriol. 178:248-257(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RT Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RT Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RT McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RT Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RT Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RT Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of *Thermotoga maritima*".
RL Nature 393:323-329(1999).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----
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CC -----
DR EMBL: X85171; CA55945.1; -
DR EMBL: AE001690; ADW35113.1; -
DR HSSP: O70351; 1E6W.
DR TIGR: TM0019; -
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Hypothetical protein; Oxidoreductase; NADP; Complete proteome.
FT NP_BIND 9 33 NADP (BY SIMILARITY).
FT ACT_SITE 153 153 BY SIMILARITY.
FT CONFLICT 130 136 RGGGVTI -> TRMSDH (IN REF. 1).
SQ SEQUENCE 236 AA; 28078 MW; D68160B1D7980C6B CRC64;
Query Match 29.7%; Score 383; DB 1; Length 256;
Best Local Similarity 35.5%; Pred. No. 2.9e-24;
Matches 93; Conservative 48; Mismatches 95; Indels 26; Gaps 7;
OY 5 LDGVAITGGLGILAIATKFEVGAQVMTDHRSDVG--EKAASVGTPODIOFQ 61
DB 2 LEGKVAVTGGGGGIGAIQAQFAENGKQVIAETDEAGVREMLERGL--DYTVK 59
OY 62 HDSSEDDWTLFLDTEAFGPVSTLVNNAAGIAVANKSVETTTAEMRLLAVNLGVEFG 121
DB 60 TDVADENSVMKVRRTVEIYGGVDVLVNNAAVMYSKSFIERPLEMERIVRNLTGPIC 119
OY 122 TRLGIORKNKGLASIIINSGSIEGFVDPGLAVNASKAGVRINSKAALDKADYD 181
DB 120 SYCAEEMIKRG--GGVITINASTRAFOSEPTEPYSASKGGLVALTJHSLAV--SLSRVHI 176
OY 182 RVNTVHPGYIKPTLVLDLFGAEAMSORTKT-----PMGHIGPNPIATYCVILA 231
DB 177 RVVSIISPMIEI-----SEMKKKSLAKKRPDLRPHDEHPAGRVGNPLDIATLCVELA 229

OY 232 SNE-SKEATGSEFVVDGCTAQ 252
DB 230 DDEKAGFTGTGNFTVDCGMIVK 251
RESULT 6
YD50_MYCTU STANDARD; PRT; 247 AA.
AC ID YD50_MYCTU
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative oxidoreductase RV1350 (EC 1.-.-.-).
GN FABG2 OR RV1350 OR MT1393 OR MYCT02B10.14.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holtroyd S.,
RA Horsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skellon S., Squares S., Squares R.,
RA Stulson J.E., Taylor K., Whitehead S., Barrell B.G.;
RA "Deciphering the biology of *Mycobacterium tuberculosis* from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
CC [2]
CC SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishal W.;
RT "Whole genome comparison of *Mycobacterium tuberculosis* clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----
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CC -----
DR EMBL: Z75555; CA99983.1; -
DR EMBL: AE007012; AAK45656.1; -
DR HSSP: O70351; 1E3S.
DR TIGR: MT1393; -
DR Tuberculist; RV1350;
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
FT NP_BIND 9 34 NAD (BY SIMILARITY).
FT ACT_SITE 155 155 BY SIMILARITY.
SQ SEQUENCE 247 AA; 25871 MW; 76CA07892E7BBA73 CRC64;
Query Match 29.5%; Score 380; DB 1; Length 247;
Best Local Similarity 36.2%; Pred. No. 4.8e-24;
Matches 92; Conservative 52; Mismatches 94; Indels 16; Gaps 4;


```

OY 1 MSNRDGLKVAIIITGTLGIGLAIAATKFEVEGAKVMITDRHSVDGEKAAKSVGTPDQIOFF 60
    1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
    1 MASLNATTAITGGAOGIGLAIGOFVAGARVVGADVLLEATEVAAKRLGDDVALAV 60
    61 OHDSDEGCMTRKLPDTEKAFGPVSTLVNAGIAVNVKSVEETTAERKLLAVNLDQVFF 120
    61 RCDVTQADVDILITFAVERFGGLDVNNAAGITRDATMTTTEBOFDVIAVHLKGTWN 120
OY 121 GTRLGIQRMKNKGLASIIIMSSIEGFVGDPSLGAYNASKAVRINSKSAALDCLKDYD 180
    121 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
    121 GTRLAALIMREKKRGA-IVNMSSVSGKVMVGOTNYSAAKAGIVGMTKAKE--LAHLG 177
OY 181 VRVNTVHGKTKPLVDLPCEAEMSQR-----TKTPMGHIGEPNDIAYICVYLAASNE 234
    181 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
    178 IRVNAIAAGLARSAMT-----EAMPORIMQKLAIEVPMGRAGESEVASAVAFLASDL 230
OY 235 SKFATGSEFVVDG 248
    235 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
    231 SSMYGTIVLDVTGG 244

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RESULT 7

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DHG1_BACME
ID DHG1_BACME STANDARD: PRT: 261 AA.
AC P39482;

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DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Glucose 1-dehydrogenase I (EC 1.1.1.47) (GLDH-1).
DE GDI.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN 11
RP SEQUENCE FROM N.A.
RA STRAIN-1AM 1030;
RA Mitamura T., Ebora R.V., Nakai T., Makino Y., Negoro S., Urabe I.,
RA Okada H.;
RT "Structure of isozyme genes of glucose dehydrogenase from Bacillus
RT megaterium 1AM1030."
RL J. Ferment. Bioeng. 70:363-369(1990).
CC -1- FUNCTION: MAY PLAY SOME ROLE IN SPORE GERMINATION.
CC -1- CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+) -> D-glucose-1,5-
CC lactone + NAD(P)H.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING SPORE germination.
CC -1- MISCELLANEOUS: PREFERS NADP TO NAD.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.

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DR EMBL; D90043; BAA14099.1;
DR PIR; J50385; J50385.
DR HSSP; P50163; 2AE1.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NADP; Multigene family; Sporulation; Germination.
FT NP_BIND 11 35 NADP (BY SIMILARITY).
FT ACT_SITE 158 158 NADP (BY SIMILARITY).
SQ SEQUENCE 261 AA; 82817 MW; B92B72B89A160335 CRC64;

```

```

Query Match 28.8%; Score 371.5; DB 1; Length 261;
Best Local Similarity 34.2%; Pred. No. 2, 5e-23;
Matches 88; Conservative 51; Mismatches 105; Indels 13; Gaps 5;

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```

OY 1 MSNRDGLKVAIIITGTLGIGLAIAATKFEVEGAKVMITDRHSVDGEKA-----AKSVGRP 54
    1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
    1 MYKDEGKVVITIGSTGKAMAIKFAFEKAKVNVNYSKE--EENSVLEEKIKV-- 56
OY 55 DOIQFQHDSDSDGCMTRKLPDTEKAFGPVSTLVNAGIAVNVKSVEETTAERKLLAVN 114
    55 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
    57 GEIAVKGVDVGVESDVINLVQSSIKKEFGKLDVINNAGMENPVSSHEMSLSDNNKAYIDN 116
OY 115 LDGFFGTRGLQRMKNKGLASIIIMSSIEGFVGDPSLGAYNASKAVRINSKSAALDC 174
    115 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
    117 LTGAFLGSRKAIKRYVENDIKGTIVNMSSVHEKIPPLVYHAASGGMKMLMETLLEY 176
OY 175 ALKDYDVRVNTVHGKTKPL-VDDLPGAEEAEMSQRKTTPMGHIGEPNDIAYICVYLAASN 233
    175 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
    177 APK-GIRVNNIGPGAINTPINAKEKADPEGRADVESMIPMGVIGPEETIAAVALASS 234
OY 234 ESKFATGSEFVVDG 250
    234 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
    235 EASYVTGITLPADGGMT 251

```

RESULT 8

```

DHG1_BACME
ID DHG1_BACME STANDARD: PRT: 261 AA.
AC P40288;

```

```

DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Glucose 1-dehydrogenase (EC 1.1.1.47).
DE Bacillus megaterium.
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN 11
RP SEQUENCE FROM N.A., SEQUENCE OF I-29, AND MUTAGENESIS.
RA STRAIN-1MG3;
RA MEDLINE=89197943; PubMed=2495285;
RA Makino Y., Negoro S., Urabe I., Okada H.;
RT "Stability-increasing mutants of glucose dehydrogenase from Bacillus
RT megaterium 1MG3."
RL J. Biol. Chem. 264:6381-6385(1989).

```

```

CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING SPORE germination.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.

```

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DR EMBL; J04805; AAA22475.1;
DR PIR; A3528; A3528.
DR HSSP; P50163; 2AE1.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NADP; Multigene family; Sporulation.
FT NP_BIND 11 35 NADP (BY SIMILARITY).
FT ACT_SITE 158 158 NADP (BY SIMILARITY).
FT MUTAGEN 96 96 E->A; G; K; HEAT STABLE.
FT MUTAGEN 108 108 D->N; HEAT STABLE.
FT MUTAGEN 112 112 V->A; HEAT STABLE.

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FT MUTAGEN 133 133 E->K: HEAT STABLE.
 FT MUTAGEN 183 183 V->I: HEAT STABLE.
 FT MUTAGEN 194 194 P->Q: HEAT STABLE.
 FT MUTAGEN 210 210 E->K: HEAT STABLE.
 FT MUTAGEN 217 217 Y->H: HEAT STABLE.
 FT MUTAGEN 252 252 O->L: HEAT STABLE.
 FT MUTAGEN 253 253 Y->C: HEAT STABLE.
 FT MUTAGEN 258 258 A->G: HEAT STABLE.
 SQ SEQUENCE 261 AA: 28085 MW: C23AC98D304EEB2F CRC64;

Query Match 28.7% Score 370.5; DB 1; Length 261;
 Best Local Similarity 33.6%; Pred. No. 3.1e-23;
 Matches 86; Conservative 51; Mismatches 108; Indels 11; Gaps 4;

OY 1 MSNRDGVKVAITGCTGIGLAIATKFEVEGAKVITP-----DRHSDGKKAASVGPDP 55
 DB 1 MYKDEGKVVITGSGTGKSKAIFATKAVVYVRKSKEDANSYLEIKKVGGEAT 60
 OY 56 QIQFQHOSSDEDGWTKLFDATKAFGPVSTLVNAGIAVNSVEETTTAEKRLAVNL 115
 DB 61 AV---KGVTVESDVINTVQSAIKKEGKLDVMINNAGLEPNVSSHEKSLDMNKVDTNL 117
 OY 116 DQVFGTRIGRMRKNGKASIIINSSIEGFVGDPSLGAVNSKAVRINSKSALDCA 175
 DB 118 TGAFLGSREAIYFVENDIKGVINNSVHEKIPWPLEFVHYASKGKMLTETLAEYA 177
 OY 176 LKDYDVRVTVHPGYIKTLP-VDDLPGAEAMSQRTKTPMGHIGEPNDIAYICVYIASNE 234
 DB 178 PK--GIRVNNIGPGAINPINKAFADPEORADVESMIPMGVIGEPETIAVAAMALASSE 235
 OY 235 SKFAAGSEFVVDGCT 250
 DB 236 ASYVTGITLFLADGCMT 251

RESULT 9

3BHD_COMTE ID 3BHD_COMTE STANDARD: PRT: 253 AA.

AC P19871;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 3-beta-hydroxysteroid dehydrogenase (EC 1.1.1.51).
 OC Comamonas testosteroni (Pseudomonas testosteroni).
 OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
 OX NCBI_TaxID=285;
 RN RN
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 11996;
 RX MEDLINE-93176721; PubMed-8382516;
 RA Adalain J.H., di Stefano S., Amet Y., Quemener E.,
 RA Adalain-Colloc M.L., Floch H.H.;
 RT Cloning, DNA sequencing and expression of (3-17)beta hydroxysteroid
 RT dehydrogenase from Pseudomonas testosteroni.
 RL J. Steroid Biochem. Mol. Biol. 44:133-139(1993).
 RN [2]
 RP SEQUENCE:
 RX MEDLINE-91224127; PubMed-2026158;
 RX Yin S.-J., Vagelopoulos N., Lundquist G., Joernvall H.;
 RT Pseudomonas 3 beta-hydroxysteroid dehydrogenase. Primary structure
 RT and relationships to other steroid dehydrogenases.
 RL Eur. J. Biochem. 197:359-365(1991).
 RN [3]
 RP CRYSTALLIZATION.
 RC STRAIN-ATCC 11996;
 RX MEDLINE-96184893; PubMed-8617258;
 RA Benach J., Knapp S., Oppermann U.C.T., Haeglund O., Joernvall H.,
 RA Ladenstein R.;
 RT Crystallization and crystal packing of recombinant 3 (or 17) beta-
 RT hydroxysteroid dehydrogenase from Comamonas testosteroni ATCC
 RT 11996.
 RL Eur. J. Biochem. 236:144-148(1996).
 CC -1- CATALYTIC ACTIVITY: Testosterone + NAD(P)(+) -> androst-4-ene-3,17-

CC CC
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -1- DATABASE: NAME-Worthington enzyme manual;
 CC WWW="http://www.worthington-biochem.com/manual/H/STDH.html".
 CC -----
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 CC -----
 CC EMBL: X6379; CAA44977.1;
 DR PIR: S15390; S15390.
 DR HSSP: P19992; IHDC.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR OXidoreductase; NAD; Steroid metabolism.
 FT INIT MET 0
 FT NP BIND 0
 FT ACT_SITE 150 150 NAD (BY SIMILARITY).
 FT CONFLICT 13 14 VV -> GG (IN REF. 2).
 FT CONFLICT 39 39 N -> NE (IN REF. 2).
 FT CONFLICT 177 177 MISSING (IN REF. 2).
 FT CONFLICT 240 240 S -> G (IN REF. 2).
 SQ SEQUENCE 253 AA: 26932 MW: CE677D9021458B39 CRC64;

Query Match 28.7% Score 370.5; DB 1; Length 253;
 Best Local Similarity 35.6%; Pred. No. 3.2e-23;
 Matches 89; Conservative 49; Mismatches 102; Indels 10; Gaps 6;

OY 2 SNRDLGKVAITGCTGIGLAIATKFEVEGAKVITPDRHSDGKKAASVGPDPDIOFQ 61
 DB 1 TNRLOGKVALVTVASGVGLGKLGAKVAFSDINA-AGQOLAELG--ERSMFR 57
 OY 62 HDSDEGCTKLFDATEKAFGPVSTLVNAGIAVNSVEETTTAEKRLAVNLGDFVFG 121
 DB 58 HGVSSPADTTLVMAAQRRLGTNLVNLNAGIILLPGMETGRLLDFSLRLINTEFVIG 117
 OY 122 TRLGQRMNKGKASIIINSSIEGFVGDPSLGAVNSKAVRINSKSALDCAKDIDV 181
 DB 118 COGIAAME--TGSIIINNASVSMPLIPQYAGYASAKAASALTRMAALSCROGYAI 175
 OY 182 -RVNTVHPGYIKTLPVD-DLP--GAEEAMSQRTKTPMGHIGEPNDIAYICVYIASNEK 236
 DB 176 RRVNSIHPPGCTTPPMQASLPKGVSKEMVLDRLNRAGRAYMPERIAQLVFLASDESS 235
 OY 237 FATGSEFVVD 246
 DB 236 VMSGSELHAD 245

RESULT 10
 FBAG_THEME ID FBAG_THEME STANDARD: PRT: 246 AA.
 AC Q9X248;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 3-oxoacyl-(acyl-carrier protein) reductase (EC 1.1.1.100) (3-ketoacyl-
 DE acyl carrier protein reductase).
 GN FBAG OR Fm1724.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogae; Thermotogales;
 OC Thermotogaceae; Thermotoga.
 OX NCBI_TaxID=2336;
 RN RN
 RP SEQUENCE FROM N.A.

```

OC Bacteria;Firmicutes; Bacillales; Bacillaceae; Bacillus.
RN NCBI_TaxID=1404;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=M1286;
RX MEDLINE=88271315; PubMed=3134196;
RA Hellmann H.J., Maegerl H.J., Gassen H.G.;
RT Identification and isolation of glucose dehydrogenase genes of
RL Bacillus megaterium M1286 and their expression in Escherichia coli.;
RL Eur. J. Biochem. 174:485-490(1988).
CC -1 CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+) -> D-glucono-1,5-
CC lactone + NAD(P)H.
CC -1 SUBUNIT: HOMOTETRAMER.
CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC
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CC
CC
DR EMBL, X12370; CA30931.1; .
DR PIR, S00812; S00812.
DR HSSP; P50162; 1AE1.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS; PRO0080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NADP; Multigene family.
FT NP_BIND 11 35 NADP (BY SIMILARITY).
FT ACT_SITE 158 158 BY SIMILARITY.
SQ SEQUENCE 261 AA; 28187 MW; 6FADADA3968DC417C CRC64;

Query Match 28.28; Score 363.5; DB 1; Length 261;
Best Local Similarity 31.5%; Pred. No. 11e-22;
Matches 82; Conservative 51; Mismatches 108; Indels 19; Gaps 4;

OY 1 MSNRLDKQVAILTGGTGLIGLAITNKFVEBAAKMIT-----DHSVQGEAAASV 51
DB 1 MYTDKDKDVAIVTGGSGTGLGRAMAVRFGQEBAAKAVINYNNNEEALDKKKEVEAGGAI 60
OY 52 GTPDOIOFFQHDSDDEDEGWTKLFPDATEKAFGPVSTLVNAGIAVANKSVEETTPAEMRKLL 111
DB 61 -----IYQSDVYKKEEDVNVLYQTAKEPFTLDVIMNNGVEMPVPSHELSLDNNKNAVY 113
OY 112 AVNDGVFEFTGLGCIQRKRNKGLGASTIINMSISIEGFWGDSPLGAVYNSKAGVRIKSSAA 171
DB 114 DTNLTGAFGLGSRERAIKFEVENDIKGVYINMSVHEMIPWPLFVHYASKGCMKLTETELA 173
OY 172 LDCAKQDYDVNVNVHGGYIKITPL-VDDLPAEEAMSDRTPPGHIGEPNDIAYICYLL 230
DB 174 LEIVAPK-GIVNVNIGPAMNTPIINAEKFADEQRADEVSMIPMGYIGKPEVAVAFAFL 231
OY 231 ASNESKEFATGSEFVVDGYYT 250
DB 232 ASSQASVYTGITLFPADGGMT 251

RESULT 12
DHGB_BACME
AC ID DHGB_BACME STANDARD; PRT; 262 AA.
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Glucose 1-dehydrogenase B (EC 1.1.1.47).
GN GDHB
OS Bacillus megaterium.
CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1404;

```

Qy	116	DCGFGTGLGICORHKNKGLGSLINMSI-EGCFGDPSLCAYANVAGAVINMSKALDC	174
Db	119	TCAGFLGSNEALKIYVENDICKGTIVINMSVHEMKIIPMLPFLHYAASGGKMLTETLALCY	178
Qy	175	ALKDYDVAVNTVHPGQIKYKTP-LVDLPGAEASMSQRTKTPMGHIGEPNDIAYICVYLA	233
Db	179	APK-GIYVNNIGGCAINTPINEKEFADPEQADVEDSMIPMGYIGEPERIAAV-AMLA	235
Qy	234	ESKFATGSEFVDDGGYT	250
Db	236	EASVYTGITLFPADGCMT	252

RESULT 13			
ID	DHG_BACSU	STANDARD;	PRT; 261 AA.
AC	PI21310: P944330;		
DT	01-OCT-1989 (Rel. 12, Created)		
DT	30-MAY-2000 (Rel. 39, Last sequence update)		
DE	15-JUN-2002 (Rel. 41, Last annotation update)		
GN	Glucose 1-dehydrogenase (EC 1.1.1.47).		
GN	GDH.		
OC	Bacillus subtilis.		
OC	Bacteriat; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OC	NCBI_TaxID=1423;		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-168;		
RA	MEDLINE=66168021; PubMed=3082854;		
RA	Lampel K.A., Uralant B., Chaudhry G.R., Ramaley R.F., Rudnikoff S.;		
RT	"Characterization of the developmentally regulated Bacillus subtilis		
RT	glucose dehydrogenase gene.";		
RL	J. Bacteriol. 166:238-243(1986).		
RN	(2)		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-168;		
RA	MEDLINE=971214189; PubMed=8969502;		
RA	Yaman K., Kumano M., Kurita K.;		
RT	"The 25 degrees-36 degrees region of the Bacillus subtilis chromosome:		
RT	determination of the sequence of a 146 kb segment and identification		
RL	of 113 genes.";		
RL	Microbiology 142:3047-3056(1996).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-168;		
RA	MEDLINE=98044033; PubMed=9384377;		
RA	Kunst F., Ogašwara N., Mosser I., Albertini A.M., Alloni G.,		
RA	Aaevedo V., Belterio M.G., Bessières P., Bolotin A., Borchert S.,		
RA	Boritis R., Boursier L., Brans A., Braum M., Brigelli S.C., Bron S.,		
RA	Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,		
RA	Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,		
RA	Daniot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,		
RA	Enlian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,		
RA	Flitz S.Y., Glaeser P., Goffeau A., Golligly E.J., Grand G.,		
RA	Guiseppi G., Guy B.J., Haga K., Hsieh J., Harwood C.R., Henaut A.,		
RA	Hilbert H., Holsappel S., Hosono K., Hulio M.F., Itaya M., Jones L.,		
RA	Joris B., Karamata D., Kasahara Y., Kleaer-Blanchard M., Klein C.,		
RA	Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,		
RA	Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,		
RA	Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,		
RA	Medina N., Mellado R.P., Mizuno M., Mosti D., Nakai S., Noback M.,		
RA	Noone D., O'Reilly M., Ogawa K., Ogilvie A., Oudega B., Park S.H.,		
RA	Parro V., Pohl T.M., Portetelle D., Porrolik S., Pisscott A.M.,		
RA	Pescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,		
RA	Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadle Y.,		
RA	Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,		
RA	Sekiuchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,		
RA	Sorokin A., Taccoli E., Takagi T., Takahashi H., Takemaru K.,		
RA	Takeuchi M., Tamakoshi A., Tanaka T., Terpsita P., Tognoni A.,		
RA	Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassartoli A.,		
RA	Viari A., Wambut R., Wedler E., Wedler H., Weltenegeyer T.,		
RA	Winters P., Wipat A., Yamamoto H., Yaman K., Yasumoto K., Yata K.,		
RA	Yoshida K., Yoshikawa H.F., Zumslein E., Yoshikawa H., Danchin A.;		

*The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 RT subunit.1; Nature 390:249-256(1997).
 RL -1- CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+) -> D-glucono-1,5-lactone + NAD(P)H.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- INSTRUCTION: IT IS INDICED AT STAGE III OF THE SPOULATION.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
 CC -----
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 CC -----
 CC EMBL: M12276; AAA22463.1; -
 DR EMBL: D50453; BAA09024.1; -
 DR EMBL: 299106; CAB12201.1; -
 DR PIR: S36090; S36090.
 DR HSSP: P50162; IAE1.
 DR Subtilist: BG10545; gdh.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT.1.
 DR Oxidoreductase: NADP; Sporulation; Complete proteome.
 FT NP_BIND 11 NADP (BY SIMILARITY).
 FT ACT_SITE 158 158 BY SIMILARITY.
 FT CONFLICT 148 150 EVI -> AF (IN REF. 1).
 FT SEQUENCE 261 AA; 28090 MW; 5894C17DB8F14965 CRC64;
 SO
 Query Match 27.8%; Score 358.5; DB 1; Length 261;
 Best Local Similarity 33.9%; Pred. No. 2.9e-22;
 Matches 87; Conservative 45; Mismatches 104; Indels 21; Gaps 5;
 QY 5 LDGKVAITGGTGLGIGLAIAATKFEVEEGAKVMIT-----DRHSDVGEKAAKSVGTPDOIOF 59
 DB 5 LKGVVAITGAASGLGKAMAFRFGKQAKVINYSNKQDNEVEKVEYIKAGC---ENVV 61
 QY 60 FOHDSDEGCKTKLPATEKAFGPVSTLVNNAAGAVNKSVEETTTAEKRLKLAIVLDGVE 119
 DB 62 VOGDVTKKEEDVKNIVYOTAIKEFGTLDIMNAGLENVPVPSHEMLKDWKVIYGTNLGAF 121
 QY 120 FCTRLGIGQMKKNGLGASIIINMSSIEGFGVDPISGAYNASKGAVRINKSALDCAIKDY 179
 DB 122 LGSRAIKIFVENDIKGVINMSSVHEVTPLEFVHYAASGGIKLMTETLALVAPK-- 179
 QY 180 DVAVNTVHPGVIKTPLVDDLPGAEEMASQRTKT-----PMGHIGEPNDIAYICVYLASN 233
 DB 180 GIRVNNIGGAIINTPI-----NAEKFAIDPKQKADVESMIPGVIYIGEPPEIAVAAMWLASK 234
 QY 234 ESKFATGSEFVVDDGTYT 250
 DB 235 EASYVTGITLFLADGGMT 251
 RESULT 14
 DHG4_BACME STANDARD; PRT; 261 AA.
 ID DHG4_BACME
 AC P39485;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Glucose 1-dehydrogenase IV (EC 1.1.1.47) (GLCDH-IV).
 GN GDBII.
 OS *Bacillus megaterium*.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1404;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-1AM 1030;
 RX MEDLINE=92332436; PubMed=1629157;
 RA Nagao T., Mitamura T., Wang X.H., Negoro S., Yomo T., Urabe I.,
 RA Okada H.;
 RT "Cloning, nucleotide sequences, and enzymatic properties of glucose
 RT dehydrogenase isozymes from *Bacillus megaterium* 1AM1030.";
 RL J. Bacteriol. 174:5013-5020(1992).
 CC -1- CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+) -> D-glucono-1,5-lactone + NAD(P)H.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- MISCELLANEOUS: PREFERRED NAD TO NADP; 2M NaCl ENHANCES ITS PH AND THERMOSTABILITY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
 CC -----
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 CC -----
 CC EMBL: D10626; BAA01476.1; -
 DR HSSP: P50162; IAE1.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT.1.
 DR Oxidoreductase: NAD; Multiligene family.
 FT NP_BIND 11 NAD (BY SIMILARITY).
 FT ACT_SITE 158 158 BY SIMILARITY.
 FT SEQUENCE 261 AA; 28157 MW; 6FBEC9397BCF17C CRC64;
 SO
 Query Match 27.7%; Score 357.5; DB 1; Length 261;
 Best Local Similarity 32.1%; Pred. No. 3.5e-22;
 Matches 85; Conservative 51; Mismatches 100; Indels 29; Gaps 6;
 QY 1 MSNLDGKVAITGGTGLGIGLAIAATKFEVEEGAKVMIT-----DRHSDVGEKAAKSV 51
 DB 1 MYDLDKRVVYITGGSTGLGRAMAVRFGQEKAVVINYNEEALDAKKEVEAGGQAT 60
 QY 52 GTPDOIOFPOHDSDEGCKTKLPATEKAFGPVSTLVNNAAGAVNKSVEETTTAEKRLKLA 111
 DB 61 -----YOGDVTKKEEDVKNIVYOTAIKEFGTLDIMNAGLENVPVPSHEMLKDWKVIY 113
 QY 112 AVNLDGVEFGTGLGIGQMKKNGLGASIIINMSSIEGFGVDPISGAYNASKGAVRINKSAA 171
 DB 114 DTMLTGAFILGSRKIKYFVENDIKGVINMSSVHEMTPLEFVHYAASGGIKLMTETLA 173
 QY 172 LDCALKRDVAVNTVHPGVIKTPLVDDLPGAE-EAMSQRKTTPMGHIGEPNDIAY 225
 DB 174 LETAAPK--GIRVNNIGGAMTPIINAEKFAIDPVORADVESM-----IPMGYIGKPEVAA 226
 QY 226 ICVYLASNESKFAFGSEFVVDDGTYT 250
 DB 227 VAAFLASSQASVYTGITLFLADGGMT 251
 RESULT 15
 DHG2_BACME STANDARD; PRT; 261 AA.
 ID DHG2_BACME
 AC P39483;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Glucose 1-dehydrogenase II (EC 1.1.1.47) (GLCDH-II).
 GN GDBII.
 OS *Bacillus megaterium*.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1404;
 RN [1]
 RP SEQUENCE FROM N.A.

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 17:13:46 ; Search time 35 seconds
(without alignments)
1483.539 Million cell updates/sec

Title: us-09-910-033a-2
Perfect score: 1290
Sequence: 1 MSNRLDGKVAITGTLGIG.....NESKFGSGFVVDGQYTAQ 252

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaeophages:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	470	36.4	261	16 09AB11	09AB11 caulobacter
2	452.5	35.1	250	2 0937L4	0937L4 comamonas t
3	438	34.0	254	16 09K4G9	09K4G9 streptomyc
4	427.5	33.1	244	2 08VL53	08VL53 xanthobacte
5	411	31.9	251	2 09RNK5	09RNK5 zymomonas m
6	411	31.9	254	2 052587	052587 comamonas t
7	395.5	30.7	256	2 0930G5	0930G5 brevibacter
8	391	30.3	249	2 056841	056841 xanthobacte
9	388	30.1	260	17 08U3B3	08U3B3 pyrococcus
10	386.5	30.0	247	2 093RM0	093RM0 acinetobact
11	386.5	30.0	251	2 09F7E0	09F7E0 acinetobact
12	378.5	29.3	258	2 09JN17	09JN17 agrobacteri
13	376.5	29.2	255	16 098E80	098E80 rhizobium 1
14	374.5	29.0	248	16 031680	031680 bacillus su
15	374.5	29.0	250	16 098C63	098C63 rhizobium 1
16	373	28.9	249	2 09L8G5	09L8G5 geobacillus

17	372.5	28.9	253	16 0930L7	0930L7 rhizobium m
18	371.5	28.8	252	16 08XW9	08XW9 raietonia s
19	370	28.7	246	2 09EX74	09EX74 rhodococcus
20	369.5	28.6	251	16 092PY8	092PY8 rhizobium m
21	368	28.5	253	16 09CH41	09CH41 lactococcus
22	367	28.4	258	16 033339	033339 mycobacteri
23	366	28.4	272	16 099RG1	099RG1 staphylococ
24	364.5	28.3	255	16 P95286	P95286 mycobacteri
25	364	28.2	264	16 09AK65	09AK65 streptomyc
26	360.5	27.9	251	2 08RG25	08RG25 fusobacteri
27	360	27.9	251	2 09FDK2	09FDK2 zymomonas m
28	359	27.8	256	16 0982N5	0982N5 rhizobium 1
29	359	27.8	269	16 08UKD8	08UKD8 agrobacteri
30	358	27.8	270	6 09MYP6	09MYP6 bos taurus
31	357.5	27.7	251	16 08UKA9	08UKA9 agrobacteri
32	357.5	27.7	258	16 0930L5	0930L5 rhizobium m
33	357.5	27.7	261	2 09F5L5	09F5L5 bacillus su
34	357.5	27.7	271	16 08ZGK4	08ZGK4 yersinia pe
35	357	27.6	296	16 09ABX6	09ABX6 caulobacter
36	356.5	27.6	248	16 08U9B5	08U9B5 agrobacteri
37	356.5	27.6	256	16 092MR3	092MR3 rhizobium m
38	353.5	27.4	255	16 08RDC3	08RDC3 thermotoga
39	351	27.2	286	16 09WYD3	09WYD3 pseudomonas
40	350	27.1	257	16 09WYD3	09WYD3 thermotoga
41	348.5	27.0	255	16 092RW7	092RW7 rhizobium m
42	347.5	26.9	268	17 09HLN6	09HLN6 thermoplasm
43	347	26.9	243	16 09KCG9	09KCG9 bacillus ha
44	346.5	26.9	254	2 09RH24	09RH24 zymomonas m
45	346.5	26.9	255	16 09WY52	09WY52 thermotoga

ALIGNMENTS

RESULT 1

09AB11 ID 09AB11 PRELIMINARY: PRT: 261 AA.

DR 01-JUN-2001 (TREMBLrel. 17, Created)

DR 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DR 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE 2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase.

GN CC0246.

OS Caulobacter crescentus.

OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;

OC Caulobacter.

OX NCBI_TaxID=155892;

RM [1]

RP SEQUENCE FROM N.A. / GB15;

RC STRAIN=ATCC 19089 / GB15;

RX MEDLINE=21173698; PubMed=11259647;

RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., DeBoy R.T., Dodson R.J., Durkin A.S., Gains M.L., Holt D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utechtbeck T., Tran K., Wolf A., Yamashiro J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M., "Complete genome sequence of Caulobacter crescentus.", Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

RT -1 (SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

CC EMBL: AE005698; AKR2233.1; -

CC HSSP: P19992; IHNC.

DR TIGR: CC0246; -

DR InterPro: IPR002198; ADH_short.

DR Pfam: PF00106; adh_short; 1.

DR PRINTS: PR00080; SDRFAMILY.

DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.

KW Oxidoreductase; Complete proteome.

SEQUENCE 261 AA: 27011 MW; CE011D872D4EBA6D CRC64;

Query Match 36.4%; Score 470; DB 16; Length 261;

Best Local Similarity 40.7%; Pred. No. 2.9e-27;
Matches 107; Conservative 46; Mismatches 90; Indels 20; Gaps 6;

QY 2 SNRLGKVAIIITGTLGIAIATKFEVGGAKVITDRHSVGEKAKSVCTPDIOQ--- 58
DB 5 TGRVAGKKAFFITGAGCAGLGAAGAKMLAKESAKVAL---ADINLAGAOVA--DEINAAH 58
QY 59 -----FEOHSSDEDEGWTKLFEDATEKAGFPVSTLVNAGIAVKKSVETTTAEEMKLLA 112
DB 59 GAGTAFAPFELDYTOEDOMIDVLEKATAAMGSLVLYNNAGIGCGPIESLDIFGLMKKVM 118
QY 113 VLDGVEFETRLGIOMKKGASIIINSSIGFVCDPBLGAYNAKSGAVRIMSKSAL 172
DB 119 VAVDSVFLLAKAHLTHMRHOPe-STIINSSITAGLIANGSPALNAKAVMLLSKINIAL 177
QY 173 DCAIKDYRVNVTVPFGYIKTPLVDLP--GAEAMSORTK-TPMGHIGEPNDIAYICV 228
DB 178 YCAKKMLDIRNSIHFTIDTPIIDGFSARFKGEAFKAKLARQVPLGRIGEPNDIANNVL 237
QY 229 YIASNESKFKATGSEFPVDDGYTA 251
DB 238 YIASDESKFMTGAETIKVDGISA 260

RESULT 2

0937L4 PRELIMINARY; PRT: 250 AA.

AC 0937L4
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
DE Cyclohexanol dehydrogenase (EC 1.1.1.1).
GN CPMB.
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
RX NCBI_TaxID=285;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NCIMB 9872;
RA van Bellen J.B., Fritzsche U., Seeger M., Smits T.H.M., Wiltolt B.;
RT "Cloning of Baeyer-Villiger monooxygenases from Comamonas,
Xanthobacter and Rhodococcus via PCR with highly degenerate primers."
RT Submitted (NOV-2001) to the EMBL/Genbank/DDI databases
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL: AJ418060; CAD10799.1;
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
KM Oxidoreductase.
SQ SEQUENCE 250 AA: 26626 MW: 76423036ABBB858E CRC64;

Query Match 35.1%; Score 452.5; DB 2: Length 250;
Best Local Similarity 38.8%; Pred. No. 5.4e-26;
Matches 97; Conservative 48; Mismatches 100; Indels 5; Gaps 4;

QY 4 RLDDGVAIIITGTLGIAIATKFEVGGAKVITDRHSVGEKAKSVCTPDIOQFQOH- 62
DB 3 RVNKKVVLVTGAMGMLTCTLLAREGATVYLSDMNEETGHOVAEIRROGCKAHLHL 62
QY 63 DSSDEGWTKLFEDATEKAGFPVSTLVNAGIAVKKSVETTTAEEMKLLAVNLDGYFPGT 122
DB 63 DVTNENHTGAVDTILAESDRIDLAVNNAGITLTKPVODTSNEEMWRIETINRSVFLGT 122
QY 123 RLGIORMKKGLGASIIINSSIGFVCDPBLGAYNAKSGAVRIMSKSALDCAIKDYRV 182
DB 123 RAVIEPMKAKHGC-IVNVSSITGLVAGAGAAAYERSKAVRLFTACAVD--LAPNIR 179
QY 183 VNVYHPGKIKTPLVDD-LPGAEAMSORTKTPMGHIGEPNDIAYICVLYASNESKFKATGS 241
DB 180 VNSVHPGIATPMTQOILDAPQSARALLGLPFLGKRAAQPMVEVSAVLFTVSDBASFVHGS 239
QY 242 EFVVDGGYTA 251
I | | | | |

DB 240 ELVVDGGYTA 249

RESULT 3

09K4G9 PRELIMINARY; PRT: 254 AA.

AC 09K4G9
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Putative oxidoreductase.
GN SC04169 OR SC066.06.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Oliver K., Harris D.;
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Redenbach M., Kleser H.M., Denapalte D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome."
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Horsby T., Howard S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2)."
RL Nature 417:141-147(2002).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL: AL358692; CAB94073.1;
DR HSSP: P19992; IHDC.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
KM Oxidoreductase.
SQ SEQUENCE 254 AA: 26132 MW: A372F691F1B8672 CRC64;

Query Match 34.0%; Score 438; DB 16: Length 254;
Best Local Similarity 40.7%; Pred. No. 6.6e-25;
Matches 100; Conservative 40; Mismatches 100; Indels 6; Gaps 4;

QY 5 LDGVAIIITGTLGIAIATKFEVGGAKVITDRHSVGEKAKSVCTPDIOQFQOHDS 64
DB 4 LTGKNVITGARGAGAEARQAVAGAVLITVDLDDGEMNARELG--DRARFLHHVD 61
QY 65 SDEGWTKLFEDATEKAGFPVSTLVNAGIAVKKSVETTTAEEMKLLAVNLDGYFPGT 124
DB 62 TSEDMRSRADEAVTEFGALHGLVNNAGISTGTPLESESDHFRKVLVNLTVGVIGMKT 121
I | | | | |

RESULT 7		
0930G5		
ID	0930G5	PRELIMINARY: PRT, 256 AA.
AC	0930G5;	
DT	01-DEC-2001 (TREMBLrel, 19, Created)	
DT	01-DEC-2001 (TREMBLrel, 19, Last sequence update)	
DT	01-MAR-2002 (TREMBLrel, 20, Last annotation update)	
DE	Cyclohexanol dehydrogenase.	
GN	CHNA.	
OS	Brevibacterium sp. HCU.	
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteriales;	
OC	Actinomycetales; Micrococccineae; Brevibacteriaceae; Brevibacterium.	
OX	NBI_TaxID-133406;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-HCU;	
RA	Brzostowicz P.C., Blasko M.S., Rouviere P.E.;	
RT	Identification of Two Gene Clusters Involved in Cyclohexanone in	
RT	Brevibacterium sp. HCU.;	
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.	
CC	-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES	
CC	(SDS) FAMILY.	
CC	EMBL: AF257214; AAK73164.1; -	
DR	InterPro: IPR002198; ADLshort.	
DR	pfam: PF00106; adh_short; 1.	
KW	Oxidoreductase.	
SO	SEQUENCE 256 AA; 26518 MW; C483D9F6BDBD1836 CRC64;	

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QY      233 NESKFATGSEFVDGGYTAQ 2522
          | : | | : | | | | |
Db      237 EEASFITGAVLPVDGCGYTAQ 2566
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RESULT	ID	AC	PRELIMINARY:	PRF:	249 AA.
056841	056841				
DT	01-NOV-1996	(TREMblrel. 01, Created)			
DT	01-NOV-1996	(TREMblrel. 01, Last sequence update)			
DT	01-MAR-2002	(TREMblrel. 01, Last annotation update)			
DE	Orf5 protein.				
GN	ORF5.				
OS	Xanthobacter sp. (strain Py2).				
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;				
OC	Phycomicrobium group; Xanthobacter.				
OX	NCBI_Taxid=78245;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-Py2:				
RX	MEDLINE=95219103; PubMed=7704278;				
RA	Saeving J., Weijers C.A.G.M., van Ooyen A.J.J., de Bont J.A.M.;				
RT	"Complementation of Xanthobacter Py2 mutants in epoxylakane				
RT	degradation: expression and nucleotide sequence of the complementing				
RL	DNA fragment."				
RL	Microbiology 141:477-484(1995).				
CC	-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES				
CC	(SDR) FAMILY.				
DR	EMBL: X79863; CAA56245.1; -.				
DR	HSSP: P19992; 1HDC.				
DR	InterPro: IPR002198; ADH_short.				
DR	Pfam: PF00106; adh_short.1.				
DR	PRINTS: PR00080; SDRFAMILY				
DR	PROSITE: PS00061; ADH_SHORT; UNKNOWN1.				
DR	Oxidoreductase.				
SO	SEQUENCE	249 AA;	24940 MW;	B5E0B82C1D8D9782	CRC64;

Query Match	30.3%;	Score 391;	DB 2;	Length 249;
Best Local Similarity	38.9%;	Pred. No. 2e-21;		
Matches	98;	Conservative	39;	Mismatches 105;
				Indels 10;
				Gaps 6

QY	5	LDGVAITITGGTIGGIAIATKPEEGAKWITDRSHSDVEKAKSVGTDPQIOFFRQHS	64
Db	2	LDAEVAITITGGAGCIGIAVAHAARIGARVAALLIDRGACACAAAEFGA--AANGADV	59
QY	65	SDEGQWTKLEDATEKAGPSTLVNNAGIVNKSVEETTTAEWRKLLAVNLIDGVFFGTRL	124
Db	60	TDEAIIATAAAGAAQORALGPLELGLVNNNGIAGFGSVHATEVETMSRIAAVAVTGTFFLASKA	119
QY	125	GIQRMKKKIGASITNNSSIEGFGDPSLCATYNAKCAVATMSKAALDCAALKDYDVRN	184
Db	120	ALFGMERGRGA-IVNGSVAGLVGIPITMAAYCAAKAVANLITROMADYSGR--GIRVN	176
QY	185	TVHGYIK-PLVLDDLPJGAE--EAMSOR-TKTPMHIGEPENIDAYICVYLASNESKAT	239
Db	177	VVPCGTAGIDMKRQLLGTDCDEPLEARRLAKIPMGKFGTIPEDIAEAAYELLSTKAAFT	236
QY	240	GSEFVVDDGTYA	251
Db	237	GSVLAVDGGMTA	248

RESULT 9

Q8U3B3

Q8U3B3

PRELIMINARY; PRT; 260 AA.

AC 08U3B3;

DT 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE 3-oxoacyl-[acyl-carrier protein] reductase.

PF0357.

Pyrococcus furiosus.

Db 237 VTGSQVYVDCAYTSK 251

RESULT 12

09JUN17 PRELIMINARY: PRT: 258 AA.

AC 09JUN17: 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)

GN YHG.

OS Agrobacterium tumefaciens.

OC Plasmid TI.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Rhizobiaceae; Rhizobium.

OX NCBI_TaxID=358;

RP [1]

RP SEQUENCE OF 1-6 FROM N.A.

RX MEDLINE-96236046; PubMed-8655509;

RA Kim K.S., Farrand S.K.;

RT "Ti plasmid-encoded genes responsible for catabolism of the crown gall

RT opine mannopine by Agrobacterium tumefaciens are homologs of the T-

RT region genes responsible for synthesis of this opine by the plant

RT tumor.";

RL J. Bacteriol. 178:3275-3284(1996).

RL [2]

RP SEQUENCE OF 4-258 FROM N.A.

RX MEDLINE-99141607; PubMed-9987134;

RA Lyl S.M., Jafri S., Winans S.C.;

RT "Mannopine acid and agropine acid catabolism region of the octopline-

RT type Ti plasmid pT115935.";

RL Mol. Microbiol. 31:339-347(1999).

RL [3]

RP SEQUENCE FROM N.A.

RX Winans S.C., Zhu J., Oger P.M., Schrammeyer B., Hooykaas P.J.;

RA Farrand S.K.;

RT "Octopline-type Ti plasmid sequence.";

RL Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES

CC (SDR) FAMILY.

CC EMBL: AF242881; AAF77146.1; -

DR HSSP: P50162; IAEI.

DR InterPro: IPR002198; ADH_short.

DR Pfam: PF00106; adh_short.1.

DR PRINTS: PR00080; SDRFAMILY.

DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.

KW Oxidoreductase; Plasmid.

SO SEQUENCE 258 AA; 27591 MW; B4EAD0364468C44C CRC64;

Query Match 29.3%; Score 378.5; DB 2; Length 258;

Best Local Similarity 37.6%; Pred. No. 1.8e-20;

Matches 97; Conservative 40; Mismatches 102; Indels 19; Gaps 6;

Db 4 RLDGKVAIIITGTLGGLATATKFEVEGAKVMTDRHSDVGEKAASVGPDPDIOGFQHD 63

Db 11 RLDGKVAIIITGTLGGLATATKFEVEGAKVMTDRHSDVGEKAASVGPDPDIOGFQHD 69

Db 64 SDEDEGKTKLEFATEKAFGPVSTLVNAGIAVNVKSVEETTAEMRKLLAVNLGCVFETR 123

Db 70 LKTRACALVYKRVADDAAGRLDILINNAGIANGDTPLEFGQMRDVIATVNEVFWCSQ 129

Db 124 LGIQRMKKGKGLASTIINNSIEGFGVD--PSLGAYNASKAGAVRIMSKAALDCAIKDYD 181

Db 130 AAIPTVMREGGRGA-IVNVGSMGSIYINIPONOVAYNSKAAVMHMKRSLASLALD--NI 186

Db 182 RVNTHPGYIKRPLVDLPGAEASQRTK-----TPMGHIGEPNDIAYICVYASNE 234

Db 187 RVNAVAPGIIIDDM-----SRGGMVHPVGRPIWLEMTPMKRFGRDEIATILFLASEA 240

Db 235 SKFATGSEFVVDGYYTAQ 252

Db 241 SSVYTGDIIVVDGYYTTR 258

RESULT 13

09BENO PRELIMINARY: PRT: 255 AA.

AC 09BENO: 01-OCT-2001 (Tremblrel. 18, Created)

DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)

DE 01-OCT-2001 (Tremblrel. 18, Last annotation update)

GN MLR4172.

OS Rhizobium loti (Mesorhizobium loti).

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Phyllobacteriaceae; Mesorhizobium.

OX NCBI_TaxID=381;

RP [1]

RP SEQUENCE FROM N.A.

RX STRAIN-MAFE30309;

RX MEDLINE-21082930; PubMed-11214968;

RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,

RA Watanabe A., Iidesawa K., Ishikawa A., Kawashima K., Kimura T.,

RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,

RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,

RA Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium

RT Mesorhizobium loti.";

RL DNA Res. 7:331-338(2000).

DR EMBL: AP003003; BAB50888.1; -

DR InterPro: IPR002198; ADH_short.

DR Pfam: PF00106; adh_short.1.

DR PRINTS: PR00080; SDRFAMILY.

KW Complete proteome.

SO SEQUENCE 255 AA; 26441 MW; 7EAF89BD46810117 CRC64;

Query Match 29.2%; Score 376.5; DB 16; Length 255;

Best Local Similarity 38.3%; Pred. No. 2.5e-20;

Matches 101; Conservative 37; Mismatches 103; Indels 23; Gaps 7;

Db 1 MSRLGKVAIIITGTLGGLATATKFEVEGAKVMTDRHSDVGEKAASVGPDPDIOGFQHD 59

Db 1 MGRRLGKVAIIITGTLGGLATATKFEVEGAKVMTDRHSDVGEKAASVGPDPDIOGFQHD 60

Db 60 FOHDSDE-DGWTKLEFATEKAFGPVSTLVNAGIAVNVKSVEETTAEMRKLLAVNLGCV 118

Db 61 FVADVDEAGVQAAGVATGATEK-LGPYVVLNHNACTIYIKPLETVOEDMLHAAVNSM 119

Db 119 FGTGRLGIQRMKKGKGLASTIINNSIEGFGVDPSLGAYNASKAGAVRIMSKAALDCAIKD 178

Db 120 FLMTAVLPGMIMAG-GGSIVCTSSISAVAAATPMEVLYDTTKGACHMFAARLAIVE-FRD 176

Db 179 YDVRVNTVHPGYIKTP-----LVVDLPGAEASQRTKTPMGHIGEPNDIAYIC 227

Db 177 RIRICNAVCPGFIPTRHGILEVADLKRIGVDSDALAQQ-----GRIGPEEVAKAA 230

Db 228 VYLAESKFAATGSEFVVDGYYTA 251

Db 231 LYLADESSFVNCALHFDVNGFTA 254

RESULT 14

ID 031680 PRELIMINARY: PRT: 248 AA.

AC 031680: 01-JAN-1998 (Tremblrel. 05, Created)

DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)

DE 01-MAR-2002 (Tremblrel. 20, Last annotation update)

GN YKVO protein.

OS Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

OC Bacillaceae; Bacillus.

OX NCBI_TaxID=1423;

RN [1]

